

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 22, 2002, 10:47:52 ; Search time 3748.51 Seconds

(without alignments)
11147.724 Million cell updates/sec

Title: US-09-787-559-1

Perfect score: 2533
Sequence: 1 ggcaccgcgctgcgcgcga.....aaaaaaaaaaaaaaaaaaaaa 2533

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.*
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36: em_hlg_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2533	100.0	2533	6 AX024729	AX024729 Sequence
2	2532.8	99.6	2632	6 AX024732	AX024732 Sequence
3	2326.6	91.9	2631	6 AX166527	AX166527 Sequence
4	1587.4	62.7	2650	10 AB020480	AB020480 Rattus no
5	1585.8	62.6	4092	10 AF106937	AF106937 Rattus no
6	1522	60.1	4498	10 MM011494	U11494 Mus muscu
7	1060.2	41.9	5115	5 AF219232	AF219232 Gallus ga
8	511.4	20.2	4868	6 AX086548	AX086548 Sequence
9	511.4	20.2	4868	9 HSM801732	AL136654 Homo sapi
10	511	20.2	5163	6 AX056393	AX056393 Sequence
11	509.8	20.1	2213	9 AK000396	AK000396 Homo sapi
12	504.8	19.9	148463	2 AC012140	AC012140 Homo sapi
13	504.8	19.9	158063	9 AP001046	AP001046 Homo sapi
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17	384.2	15.2	4321	6 AX056387	AX056387 Sequence
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19	346	13.7	4917	9 AB058763	AB058763 Homo sapi
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29	285.4	11.3	2190	6 AX056389	AX056389 Sequence
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ALIGNMENTS

RESULT	1	PAT	15-SEP-2000
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DEFINITION	Sequence 1 from Patent WO0017232.		
ACCESSION	AX024729		
VERSION	AX024729.1	GI:10184808	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 2533)		
AUTHORS	Reinartz,J., Bechtel,M., Kramer,M., Schaefer,B. and Wallich,R.		
TITLE	Regulatory protein from human keratinocytes		
JOURNAL	Patent: WO 0017232-A 1 30-MAR-2000;		
FEATURES	REINARTZ JEANETTE (DE) ; BECHTEL MICHAEL (DE) ; KRAMER MICHAEL (DE)		
SOURCE	; SCHAEFER BIRGIT (DE) ; WALLICH REINHARD (DE)		
	Location/Qualifiers		
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RESULT 2
AX024732 2632 bp DNA PAT 15-SEP-2000
LOCUS AX024732
DEFINITION Sequence 4 from Patent WO0017232.
ACCESSION AX024732
VERSION AX024732.1 GI:10184809
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
  1 (bases 1 to 2632)
  Rehnert,J., Bechtel,M., Kramer,M., Schaefer,B. and Walllich,R.
  Regulatory protein from human Keratinocytes
  Patent: WO 0017232-A 4 30-MAR-2000;
  REINHARTZ JEANETTE (DE) ; BECHTEL MICHAEL (DE) ; KRAMER MICHAEL (DE)
  ; SCHAEFER BIRGIT (DE) ; WALLICH REINHARD (DE)
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 2524; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DEFINITION	Sequence 18 from Patent WO0138503.			
ACCESSION	AXI66527			
VERSION	AXI66527.1	GI:14546872		
KEYWORDS				
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
TITLE	1 (bases 1 to 2361)			
JOURNAL	Flanagan,G.D., Whyte,D., Manning,G.S., Sudarsanam,S.S., Martinez,R.,			
FEATURES	Novel human protein kinases and protein kinase-like enzymes			
source	Patent: WO 0138503-A 18 31-MAY-2001;			
BASE COUNT	431 a 784 c 726 g 420 t			
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Db 1201 CAGTCCGCTCTCCAGGCGGAGATGAGATGTGAGCTCCAGAGCTCGGTGAGTGGCCCTTG 1260
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Db 1261 TTTCTTCCCGGTGATGTCACCTGACAGGAGTGTCTCGGCCCCGCGCTGTCTCCCAAGC 1320
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Db 1441 TCACCCGCGCTTCCACATCCACCGCCCATGTATAGTCTTCCCTCCACACGGCA 1500
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Db 1921 CAGCGGCGGCGAGCGGCGGAGCGGAGGCTGTGAGCTGTGAGAGTGTGTAGAGCAG 1980
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Db 2101 CCCAGCACCTCTCTCAGGTGGGCTCCCGTGTCTGCCGCCCTCTGCAACACCGGC 2160
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Db 2341 ACCTTGTCTGT 2361

RESULT 4
AB020480
LOCUS AB020480 2650 bp mRNA ROD 06-AUG-1999
DEFINITION Rattus norvegicus mRNA for salt-inducible protein kinase, complete cds.
ACCESSION AB020480
VERSION AB020480.1 GI:5672675
KEYWORDS SIK; salt-inducible protein kinase.
SOURCE Rattus norvegicus (strain: Sprague-Dawley) 6 week old male adrenal gland cDNA to mRNA.

ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (sites)

REFERENCE Wang, Z., Takemori, H., Halder, S. K., Nonaka, Y. and Okamoto, M.
TITLE Cloning of a novel kinase (SIK) of the SNF1/AMPK family from high
salt diet-treated rat adrenal
JOURNAL FEBS Lett. 453 (1-2), 135-139 (1999)
MEDLINE 99330184
REFERENCE 2 (bases 1 to 2650)
AUTHORS Wang, Z.
TITLE Direct Submission
JOURNAL Submitted (25-NOV-1998) to the DDBJ/EMBL/GenBank databases.
Zhi-nong Wang, Osaka University Medical School, Dept. Molecular
Physiological Chemistry; 2-2 Yamadaoka, Suita, Osaka 565-0871,
Japan (E-mail: wzongemr-mbio.med.osaka-u.ac.jp, Tel:81-6-879-3286,
Fax:81-6-879-3289)
COMMENT Sequence updated (28-Apr-1999).
FEATURES
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1..2650
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BASE COUNT 564 a 820 c 717 g 549 t
ORIGIN

Query Match 62.7%; Score 1587.4; DB 10; Length 2650;
Best Local Similarity 79.3%; Pred. No. 2.2e-288;
Matches 1995; Conservative 0; Mismatches 461; Indels 61; Gaps 7;

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QY 74 ccacgagaagccctccggtgggttttttaacacatcgagcgagcccttggaagcaaa 133
DB 122 CCACGAGAAAGCCCTCCGGGTGGGCTTTTACGACGCTGGAACGAAACCTGGGCAAGGCAA 181

QY 134 ctgcgagtggtgaagctgagcgagcatcgagtcaccaaagcgaagcttgcaataaaat 193
DB 182 TTTTGCAGTGGTTAAAGCTGGCGCGCACGAGTCACCAAAAGCAGGTTCGAATTAAT 241

QY 194 aattgataaaacagatataagcaatttggaagaaatctatcgttgaagttcagct 253
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QY 314 catgcttcacgtcgaacgaatttgctaaatgagaatggttatttatttacttc 373
DB 362 CATCTGTCATTTGTCACGAGATTTGCCCAAAATGAGAAAGTTGCTGATCTTCATTC 421

QY 374 caacggcaccctgaatggaacagagcgaggaagttctgcaaatccgttcgcgt 433
DB 422 CAACGGGACCTTGAGTGAAGAAAGAGAGCTAAGAAATTTGCGATCTCTCAGCCGT 481

QY 434 ggaagtactgtaacgaacatcaatcgtccacccggagacctcaagacgaacctcgt 493
DB 482 GGAGTACTGCCCACAACATCATCATGCTCACCGGGACCTTAAAGACAGAAACCTTGCT 541

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DB 542 GGACGGCAACATGACATCAAGCTGGCAGATTGGAATTTGGAAATTTCTAACAGCCAG 601

QY 554 agagcctctgtccacgltgltggaagcccccgtatgccccggagagctttgagg 613
DB 602 GGAGCCTGCTACTACTTGTGTGGAGCCCCCTATGCTCTCCCAAGCTTTGAGG 661

QY 614 gaagagatataagcccccaagctggaacatctggaagcctggggcgttgctgactct 673
DB 662 GAAGGATATGAAGTCCCCAGCTGGACATCTGAGGCTCCGCTGCTGATGCT 721

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DB 722 GGTCTGTGCTCCCTCCCTTTTGAATGAGCCCAACCTGCTACGCTGAGACAGCGGTCT 781

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QY 794 catgctggtgtggaaccccgagcgacatcacatctgcacagatcccgagacaggtg 853
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QY 1085 ccgagcccgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcg 1144
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QY 1145 gactcaggaaggtcttccacagacccttccgacctgtctgtgtgctgcgcagcgaga 1204
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D	b	1499	GGCTGAAGTTCACACCACTTCTCCCGCTCAACCCCTTCCTCAATATGTCTCTCTC	1558
O	y	1505	caccaagcgcaagttctcgcagaaggaaocagctctgcaattctcgaactctcggag	1564
D	b	1559	TGCCGCTGTGAATCCCTCGGAGAGAACTATGACTGTGACACTCTCCCTTCTGCAAG	1618
O	y	1565	caaaagcccgcgaggtctcagtgcaaccccgagcaccatcaagggcgctgtagcgctgctc	1624
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D	b	1739	TCAGGCAAGTCTGGGTCTCGACTGTCTTACTCTCTGTACACTTCCAGAGGAGCGAGAGC	1798
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D	b	1799	GTCGGATATACGTCCTCTCACTCAAGGGCGAAGGCTTCCGGGACAGCATAGGAAAAACGC	1858
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O	y	1865	gtctccctgcaagccgggcagcagaaggcgagcctcaagccctcagcgccctgcagag	1924
D	b	1919	G---TCTCTCATCCGAGGTTCCGGGGAGGATGAATACCTTTCACACCCCGGCCAAG	1975
O	y	1925	cccaagcctctgacgycgagcagcagcgagcagcgagagcttgtagccttgtagaagagt	1984
D	b	1976	CTCAGGTCGTGCAGAGCGTGCAGCGGCAAGCATGCCGAGGGCAGAGACTGTGAAAGAGT	2035
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D	b	2036	GCTGCACACGACGAGCGCTGCTCCAGTTACAGCACCTCAGCGCTCATCTGACTATACCA	2095
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D	b	2147	-----CCTTCTCGTGTGTGAATCCACTGCTGCCAGACGCCCTCTCT	2188
O	y	2165	gcgaacccgycgctcccccgttgacctcaagcgcgcagcctctgtgacaacacacttgacat	2224
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D	b	2249	CAGTGTGGGCCACTGTGCCCTTCCCACTGTGCTCCCTGCACAGTCACTCACAGGCTTTC	2308
O	y	2282	cccaagtttgtagccctctgggctgtctgcagagggagacttgagatgtagggagactgagc	2341
D	b	2309	CCCAAGCTGTATCTCTTGCTGGCTGCCGCGAGGGGGAATTGTGATGAGAGACTGTACCTC	2368
O	y	2342	ctgtccctctagcaagcttgcttccctggtgcaatgtagagcagccctgcatactctgcaagac	2401
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Oy 2446 gccctaaagccaagaacttcttagaagcgaataaagcaatcgcgttaggtctttgccc 2502
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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RESULT 5

AF106937

LOCUS AF106937 4092 bp mRNA ROD 01-DEC-1999

DEFINITION Rattus norvegicus protein kinase KID2 (KID2) mRNA, complete cds.

ACCESSION AF106937

VERSION AF106937.1 GI:6492127

KEYWORDS

SOURCE Norway rat.

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine;

Rattus.
Rattus.
1 (bases 1 to 4092)
Feldman,J.D., Vician,L., Crispino,M., Hoe,W., Baudry,M. and
Herschman,H.R.
The Kid2 gene encodes a protein kinase induced by depolarization in
brain

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 4092)
AUTHORS Feldman,J.D., Vician,L., Crispino,M., Hoe,W., Baudry,M. and
Herschman,H.R.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-1998) Pediatrics, UCLA, 10833 Le Conte Ave., Los
Angeles, CA 90095-1752, USA

FEATURES
source
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BASE COUNT 856 a 1161 c 1102 g 973 t

ORIGIN

Query Match 62.6%; Score 1585.8; DB 10; Length 4092;
Best Local Similarity 79.2%; Pred. No. 4,1e-288;
Matches 1994; Conservative 0; Mismatches 467; Indels 61; Gaps 7;

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Db 120 GCCCGAAGCAGTGTGATCATCTCGAGTTCAGGCCGGTCCCAACAGCACCGCCAGAGG 179

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Oy	2402	actgaactc-----ttacaacataacttcagagaagtgaga----cactg	2445
Db	2487	CCCAACCCACGAGATGACTCTTCACAAAGCAAAATATTTAGAGTATGTGAAGATGTTTCGG	2546
Oy	2446	gacctaaagcccaagactcttcagagaaggaataagcaatacgttaggtgtgttggc	2502
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RESULT	6		
LOCUS	MU011494		
DEFINITION	MU011494 4498 bp mRNA	ROD	29-OCT-1999
ACCESSION	Mus musculus protein kinase mRNA, complete cds.		
VERSION	U11494		
KEYWORDS	U11494.2 GI:6137751		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
TITLE	1 (bases 1 to 1434)		
JOURNAL	Ruiz,J.C., Conlon,F.L. and Robertson,E.J.		
MEDLINE	Identification of novel protein kinases expressed in the myocardium		
REFERENCE	Mech. Dev. 48 (3), 153-164 (1994)		
AUTHORS	2 (bases 1 to 1434)		
TITLE	Ruiz,J.C.		
JOURNAL	Direct Submission		
REFERENCE	Submitted (27-JUN-1994) Joseph C. Ruiz, Molecular and Cellular		
AUTHORS	Biology, Harvard University, 16 Divinity Ave, Cambridge, MA 02138,		
TITLE	USA		
JOURNAL	3 (bases 1 to 4498)		
REFERENCE	Ruiz,J.C.		
AUTHORS	Direct Submission		
TITLE	Submitted (28-OCT-1999) Wells Center for Pediatric Research, Riley		
JOURNAL	Hospital for Children, Indiana University School of Medicine, 702		
REFERENCE	Barnhill Drive, Room 2616, Indianapolis, IN 46202, USA		
AUTHORS	Sequence update by submitter		
TITLE	On Oct 28, 1999 this sequence version replaced gi:595420.		
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	AAITYLDERLKERHSAQPSRTPPATPRQQLSSDLSLEVEQLPCDPEFSPILL		
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	ROGSLSEEDQVEPLRGSTGRHRTTAEVYHFSPLNPPCIYSSATASPESTSD		
	SLCPFSAEGEPAGLGSGLATPGILGTSPPVLAEPFLGOSATPVLOTAGLGTAPG		
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	GMSFTHPAPSSGLQCGTTSNRBERSLLEVLVHQRLQLQDHSTAAASGCGGQ		
	LSVPVYVAPDCDSLVSGLTPIPLTPPLQAGMSPVASAHLLDTHLSAGVAPLTPP		
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BASE COUNT	976 a 1244 c 1075 t		

[illegible]

Db	1080	CGACCGGAGGGACCTATAGAGTCTCGCAGAACACACACTACACACACTTGGCCGCAT	11330
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Db	1140	TTACTACTCTCTACTCTCAGGCGCTCAAGAGAGATTCGACAGCGCCCTCATTCGCCGCC	11599
QY	1085	cgagcccgagcttgcagagagcccgagcttgagcttgagactgaagtggtttgaagt	11444
Db	1200	CACCCCTGCACCCACACAGACAGCCCAAGCTCCGAAACCTGAGACTGAGAGTGTGGAGCT	12599
QY	1145	gctctagaagaagttctltccacccgaccttctcgacctgtgcttgtgcccagcgca	1204
Db	1260	TCTCTCAAAATTTCTCCCGTGGTGAACCTTTCCGGCCCTCTGCTGTGGCCACAGCCCA	1319
QY	1205	gaccttgttgagtcgctcgtctccagcgagatagagctgtgagctccagagctgtcga	1264
Db	1320	GCCCTTGCTAGTCTCTCTCGAGGCTGAGTAGACTGTGATTCACAGCTCACTTCA	1379
QY	1265	gttgacctgtgtcttcccggttgatgtcgaactcgaacgagtggttccggcccgagccgt	1324
Db	1380	---GCCCTTATTATTCGCCCTGGATACAACTGCATGAGTGTTCGGCACCATCAT	1436
QY	1325	gtccccaaagcagctgtcttgcacacagccatcagltgagagcgcaagggcgagcct	1384
Db	1437	CTCCCCACAGAGTCTGCTGGACACAGCTATCAACGAGGAGCCAGGAGGTCACAGCT	1486
QY	1385	agaagaagaagagacacagcagagatccctgtgcccagcagaagggccgaacacct	1444
Db	1497	GGAGGAGGAACAGGAGGTCCAGGAAACCCCTGCCGGAACACAGGCCGAGGACACACTT	1556
QY	1445	ggcgaagttcaccacgcgctctcccactacacgacgcatgatalagtgcttccctc	1504
Db	1557	GGCTGAATCTCCACCCATTCTTCTCCCGCTCAACCCCTTCGCAATATGTCTCTCTC	1616
QY	1505	cacacgcgaagctctcgcagagggaacagctctgacgttctgacctctcgcag	1564
Db	1617	TGCCACGGCAGTCTCCTCGAAGGAGACACACTCCGACACTCTCTCTTCGCAAG	1676
QY	1555	caaaagcccgcgaggtcagltgacaccccgagcaatcaggggtgtctgtgagccgtctc	1624
Db	1677	TGAAGGTCTCTCAGGGCTTGGAGTGGCGCCGACCCAGAGGGCTGTGGACACAGCTC	1736
QY	1625	cccggtcaaggtctggccctcgccctctctgtgtgcagcttcgcaaccccaagtgctgcagc	1684
Db	1737	TTCAGTCAAGATTGGCTCTGCGCTTCTCGGATACAGTACGACCCCTGTCTCTCAAC	1786
QY	1685	tcaagggaggtcttggaaagactgttctgtccctgtcagacttccagaggaagcgcgcgc	1744
Db	1797	TCAGGCAAGTCTGGGACACACGCTTACCTCCGTCACACTTCCAGAGGAGCGAGAGC	1856
QY	1745	gtcggacaactcaactgaactaaaggtctgaagcccttcgcaagcagctgaagaaagccac	1804
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QY	1805	ggcgacaagaaggtttcttggagctgaacaatacaaggggtcgtgctgcagagtggttgcga	1864
Db	1917	GAGGACCAAGGGGTCTCTGGGACTGAACAAGATCAAAAGGTTGGCTCGCAGGTGTCCA	1976
QY	1865	ggtccctgtcacgcccgggcagcagaggggcgagcccttccacgcgcccctgcacagag	1924
Db	1977	G---TCTCTCGTCTCAAGTCTCCCGGGGAGGATGAGTACTTCCACACCCCGGCCCAAG	2033
QY	1925	ccgaagcgtctcaagcgagcgagcagcgagccggagaggtctggaacctgctctggagaggt	1984
Db	2034	CTCCGGCCTGCAGAGCTGACACACAGCAATGGGAGGCGACGAGACCTACTTTGAAGAGT	2093
QY	1985	gctlagagcagcagaggtgtgtcaggtlaagcaca-----cccgagcgtgcgaac	2035
Db	2094	CTGTGACACAGAGGGGTGTGTCCAGTTAAGACACACACTTCTACCGCGCCCTCATC	2153
QY	2036	cgcgtgtctcccaagccccccagcagccctgtgcccgtttgtgacgccccgtgtatg	2095
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QY	2096	ccctgggagctgccccgcgtcccccagacacccctctccaaagtcgggagctcccgctgctgcgcgc	2155
QY	2211	-----CACCCTCTCTGCTGTGGAAATTCACATGCTCCAC	2246
QY	2156	cccaactcctgcagacacggcgcgctgcgcgcgtgagcctcagcggcgacagctcctgacacaca	2215
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QY	2216	ccctgcacattgycacgcggcccccaagcgcctcccgctgtgtgcccccaaac---gcctgac	2277
DB	2307	CTTGACATCTAGTCTCTGGCCCAAGTGCGCTCCCACTGGGACCCCTGCACACATGCTTAC	2366
QY	2273	cagcgctgccccagctgtgtgtagccctctgagctgctgcacaggggagactgtgagatgagga	2323
DB	2367	CAGGCTGTCCCAAGCTGTATTCACAGTGGGCTGCCACAGGGGACTGTGATGTGAGCA	2426
QY	2333	ccctgatgcctgctcctctagacagcttgtctcctgtgtgacgagtagagcagccctg	2386
DB	2427	CCTGACCTCTGGCCAGCGGGGACATTCTGCTCTGATACAGTACAGGCTGCTTG	2480

RESULT	7
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LOCUS	AF219232 5115 bp mRNA VRT 15-NOV-2000
DEFINITION	Gallus gallus qtn-induced kinase mRNA, complete cds.
ACCESSION	AF219232
VERSION	AF219232.1 GI:6760435
KEYWORDS	chicken.
SOURCE	Gallus gallus
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE	1 (bases 1 to 5115)
AUTHORS	Xia,Y., Zhang,Z., Kruse,U., Vogt,P.K. and Li,J.
TITLE	The new serine-threonine kinase, qtk, is a target of the qtn oncogene
JOURNAL	Biochem. Biophys. Res. Commun. 276 (2), 564-570 (2000)
MEDLINE	20484194
PUBMED	11027514
REFERENCE	2 (bases 1 to 5115)
AUTHORS	Xia,Y., Zhang,Z., Kruse,U., Vogt,P.K. and Li,J.
TITLE	Direct Submission
JOURNAL	Submitted (27-DEC-1999) Molecular and Experimental Medicine, The Scripps Research Institute, 10550 N. Torrey Pines Road, La Jolla, CA 92037, USA
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	/product="qtn-induced kinase"
	/protein_id="AAP28351.1"
	/db_xref="gi:6760436"
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FEATURES	Sugen, Inc. (US)
source	Location/Qualifiers 1. .5163 /organization="Homo sapiens" /db_xref="taxon:9606"
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ORIGIN	2 others

Query Match	20.28;	Score 511;	DB 6;	Length 5163;
Best Local Similarity	69.58;	Pred. No. 2.9e-86;		
Matches 707; Conservative	1;	Mismatches 306;	Indels 3;	Gaps 1

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QY	955	tcattgagacccttgagcgttgaccggaagaagacggttgaaatctactctgcaaacacgacgt	1014
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QY	1015	ataaacacttgcctgccattatctaacctccctcttgagcgcgtcacaagaagatcgcga	1071
Db	1122	ATAACCACTTGTCGCCATTATTTCTTGTTGTGAGAGCGCTCGAAATTCATCTCGGA	1178

RESULT 11
AK000396

LOCUS	AK000396	2213 bp	mRNA	PRI	22-FEB-2000
DEFINITION	Homo sapiens cDNA FLJ20389 fis, clone KATA4591, highly similar to				
	AB018324 Homo sapiens mRNA for KIAA0781 protein.				

accession AK000396
 version AK000396.1 GI:7020457
 keywords oligo capping, fls (full insert sequence).
 source Homo sapiens [tela mucosa cDNA to mRNA clone 11b.1a]

ORGANISM

REFERENCE
AUTHORS
Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K.,
1 (sites)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

TITLE
JOURNAL
REFERENCE

Subanata, T., Tanaka, T., Nakamura, Y., Isogai, T. and Sugano, S.
NEBO human cDNA sequencing project
Unpublished (2000)
2 (bases 1 to 2213)

AUTHORS Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T., Shibahara, T., Tanaka, T. and Nakamura, Y.

TITLE Direct Submission

JOURNAL Submitted (15-FEB-2000) to the NRI/EMBL Genbank database

Sugano, Institute of Medical Science, University of Tokyo, Department of Virology, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8659, Japan (E-mail:cdnald@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)

COMMENT
NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry for Biotechnology; cDNA library sequencing: Research Association for Biotechnology; cDNA library construction, 5' - & 3'-end one pass sequencing: Department of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency).

FEATURES	Location/Qualifiers
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/db_xref="taxon:9606"
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Best Local Similarity	69.5%	Pred. No. 5,7e-86;		
Matches 707; Conservative	0;	Mismatches 307;	Indels 3;	Gaps 1

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| | | | | | | | | | | | | | | | | |
Db 90 cggatggcccacagaccttcagacggcgccggccggtccgggttgaggttttaacgacattcggag 148

OY 115 gTaccctgggcaagcgaacttcgcggtgtgaagctgcgcgcgcgatcgatccaccaa 174

Db 150 GCACGCTGGCGAAGGGCAACTTCGTGTGTAAGCTGGGGCGGCACCGGATCACCACAGA 209

1/5 cycaggttcgaataaaatgataaaacacgattagattcaagcaatttgagaaaa 234

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Oy 235 tctatcgtgaggtcagctgtagaagctctcgaacccatcacacataataagcttacc 294
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Db 270 TCTATCCGAGAGTAATATGATAGTATGATAGTATGATAGTATGATAGTATGATAGT 329
Oy 295 aggttatgagaaacaagaagacatcttactcgtcactgaatttgcataaaatgagaaa 354
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Db 330 AGGTAATGGAGACCAAAAGATGTTGACCTTGACAGATGATGACCAAAATGAGACAAA 389
Oy 355 tcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 414
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Oy 415 ggcacatctctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 474
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Oy 475 agacccggaacccctctctctctctctctctctctctctctctctctctctctctctct 534
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Db 510 AAGCTGAAATCTCTCTCTGATTAACATGAAATGAAATGAAATGAAATGAAATGAAAT 569
Oy 535 ggaattctcaagtcagagagagagagagagagagagagagagagagagagagagagagag 594
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Db 570 GAAATTTCTTTAAAGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 629
Oy 595 ccccggaagctcttctgagagagagagagagagagagagagagagagagagagagagag 654
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Db 630 CCCGAGAACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 689
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Db 690 GAGTGTGCTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 749
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Oy 775 gtagagagctgtagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 834
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Oy 895 ccttctcgcagacagcttacaaccccaacctgagcagctgagcagcagcagcagcagcag 954
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Db 930 CACAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 986
Oy 955 tcatgagagacccctgagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 1014
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Oy 1015 ataacaccttctgctcattatctctctctctctctctctctctctctctctctctctct 1071
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RESULT 12
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LOCUS Homo sapiens clone RP11-10M14, WORKING DRAFT SEQUENCE, 17 unordered
DEFINITION Homo sapiens clone RP11-10M14, WORKING DRAFT SEQUENCE, 17 unordered
ACCESSION AC012140
VERSION AC012140.3 GI:7341873
KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 148463)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.

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TITLE
JOURNAL
REFERENCE
AUTHORS
Homo sapiens, clone RP11-10M14
Unpublished
2 (bases 1 to 148463)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Baran,N., Becker,L., Boguslavsky,L., Boukhalter,B.,
Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
Cooke,P., DeArrellano,K., Dewar,K., Domiano,M., Donelan,L., Doyle,M.,
Ferreira,P., FitzHugh,M., Forrest,C., Funke,R., Gage,D.,
Galagan,J., Gardy,J., Grant,G., Hago,B., Heath,R., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Lehoczky,J., Lieu,C., Locke,K., MacDonald,P., Marquis,N.,
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrum,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Testa,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,N.
Direct Submission
Submitted (20-OCT-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 30, 2000 this sequence version replaced gi:6454007.
All repeats were identified using RepeatMasker:
http://ftp.genome.washington.edu/RM/RepeatMasker.html
Smit, A.F.A. & Green, P. (1996-1997)
Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information -----
Center project name: L3106
Center clone name: 10_M14
----- Summary Statistics -----
Sequencing vector: M13; M77815: 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 135488 bases at least Q40
Consensus quality: 141694 bases at least Q30
Consensus quality: 144517 bases at least Q20
Insert size: 139000; agarose-fp
Insert size: 146863; sum-of-ctnigs
Quality coverage: 4.1 in Q20 bases; agarose-fp
Quality coverage: 3.9 in Q20 bases; sum-of-ctnigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 17 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1223 2680: contig of 1458 bp in length
* 2681 2780: gap of 100 bp
* 2781 4940: contig of 2160 bp in length
* 4941 5040: gap of 100 bp
* 5041 6346: contig of 1306 bp in length
* 6347 6446: gap of 100 bp
* 6447 9361: contig of 2915 bp in length
* 9362 9461: gap of 100 bp
* 9462 13245: contig of 3784 bp in length
* 13246 13345: gap of 100 bp
* 13346 16902: contig of 3557 bp in length
* 16903 17002: gap of 100 bp
* 17003 22603: contig of 5601 bp in length
* 22604 22703: gap of 100 bp
* 22704 30328: contig of 7625 bp in length
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* 30429 35509: contig of 5081 bp in length
* 35510 35609: gap of 100 bp
* 35610 46431: contig of 10822 bp in length

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* 58466 58565: gap of 100 bp
* 58566 73599: contig of 15034 bp in length
* 73600 73699: gap of 100 bp
* 73700 89312: contig of 15613 bp in length
* 89313 89412: gap of 100 bp
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FEATURES

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misc_feature /note="assembly-fragment" 22704..30328
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misc_feature /note="assembly-fragment" vector_side:left
misc_feature /note="assembly-fragment" 35610..46431
misc_feature /note="assembly-fragment" 46532..58465
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BASE COUNT 33669 a 37741 c 38042 g 37405 t 1606 others
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Best Local Similarity 99.6%; Pred. No. 2.4e-85;
Matches 506; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 2055 cagccgcgcctcgcgttgcgtgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 2114
DB 31295 CAGCGCGCCCTGCGCGCTGTCGTCGCGCGCGCGCGCGCGCGCGCGCGCG 31236
QY 2115 ccagagccctctcagtcgtgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 2174

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RESULT 13
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DEFINITION Homo sapiens genomic DNA, chromosome 21, clone:KB43F12, MX1-D21S171
ACCESSION AP001046
VERSION AP001046.1 GI:6693596
KEYWORDS HTG.
SOURCE Homo sapiens pre-pro-B cell clone:FLB14-14 DNA, clone_lib:Keio
BAC library clone:KB43F12.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 158063)
AUTHORS Shimizu,N., Kudoh,J. and Shibuya,K.
TITLE Homo sapiens genomic DNA, chromosome 21, clone KB43F12, MX1-D21S171
region
JOURNAL Published Only in Database (2000) In press
REFERENCE 2 (bases 1 to 158063)
AUTHORS Shimizu,N., Kudoh,J. and Shibuya,K.
TITLE Direct Submission
JOURNAL Submitted (12-JAN-2000) to the DDBJ/EMBL/Genbank databases.
Nobuyoshi Shimizu, Keio University, School of Medicine, Molecular
Biology, 35 Shinanomachi, Shinjuku-ku, Tokyo 160-8582, Japan
(E-mail:nshimizu@dm.med.keio.ac.jp, Tel:01-3-3351-2370,
Fax:01-3-3351-2370)

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FEATURES

Location/Qualifiers

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VERSION	AP001751.1 GI:7768753
SOURCE	Homo sapiens DNA.
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REFERENCE	Hattori,M., Fujiyama,A., Taylor,T.D., Watanabe,H., Yada,T., Park,H.S., Toyoda,A., Ishii,K., Totoki,Y., Choi,D.K., Soeda,E., Ohki,M., Takeda,T., Sakaki,Y., Tsudeni,S., Blechschmidt,K., Polley A., Menzel,U., Delabar,J., Kumpf,K., Lehmann,R., Patterson,D., Reichwald,K., Rump,A., Schlichabel,M. and Schudy,A. The DNA sequence of human Chromosome 21. The chromosome 21 mapping and sequencing consortium Nature 405 (6784), 311-319 (2000) 20289799
JOURNAL	2 (bases 1 to 340000)
MEDLINE	Hattori,M., Fujiyama,A., Taylor,T.D., Watanabe,H., Yada,T., Park,H.S., Toyoda,A., Ishii,K., Totoki,Y., Choi,D.K., Soeda,E., Ohki,M., Takeda,T., Sakaki,Y., Tsudeni,S., Blechschmidt,K., Polley A., Menzel,U., Delabar,J., Kumpf,K., Lehmann,R., Patterson,D., Reichwald,K., Rump,A., Schlichabel,M., Schudy,A., Zimmerman,W., Rosenthal,A., Kudon,J., Shibuska,K., Kawasaki,K., Asakawa,S., Shintani,A., Sasaki,T., Nagamine,K., Mitsuyma,S., Antonarakis,S.E., Minoshima,S., Shimizu,N., Nordstiek,G., Horlischer,K., Barandt,P., Scharfe,M., Schoen,O., Desario,A., Reichelt,J., Kauer,G., Bloeker,H., Ramser,J., Beck,A., Klages,S., Hennig,S., Rlesselmann,L., Dagand,E., Wehrmaeyer,S., Borzym,K., Gardner,K., Nizetic,D., Francis,F., Lehnach,H., Reinhardt,R. and Yasp,M.L.
AUTHORS	Direct Submission Submitted (10-APR-2000) to the DDBJ/EMBL/GenBank databases. The Chromosome 21 Mapping and Sequencing Consortium: * RIKEN Genomic
TITLE	JOURNAL

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Db 149320	GCAATTAACTTTAGAGGAGAGGTAAACATCTGTGGCTCAAAAGCCAGAACTTTCTAGAAGCG	149261			
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DEFINITION	Homo sapiens chromosome 21 clone RP11-351D2, WORKING DRAFT				
ACCESSION	AC018734				
VERSION	AC018734.3				
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT.				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				
REFERENCE	1 (bases 1 to 179556)				

AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

Waterston, R. H.
The sequence of Homo sapiens clone
Unpublished
2 (bases 1 to 179556)

DIRECT SUBMISSION

Submitted (17-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Jun 16, 2000 this sequence version replaced gi:7023168.

COMMENT

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Project Information -----
Center project name: H.NH0351D02
----- Summary Statistics -----
Sequencing vector: M13; 1008
Sequencing vector: plasmid; 08
Chemistry: Dye-Primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 170077 bases at least Q40
Consensus quality: 173263 bases at least Q30
Consensus quality: 175196 bases at least Q20
Insert size: 180000; agarose-fp
Insert size: 178656; sum-of-contigs
Quality coverage: 5.54 in Q20 bases; agarose-fp
Quality coverage: 5.64 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 10 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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* 17312 30665: contig of 13354 bp in length
* 30666 30766: gap of unknown length
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* 45153 45252: gap of unknown length
* 45253 62957: contig of 17704 bp in length
* 62957 63056: gap of unknown length
* 63056 79924: contig of 16868 bp in length
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Search completed: March 22, 2002, 13:29:28
Job time: 9696 sec

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: Patent No. 6258547			
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: APPLICANT: Berl, Rajinder K.			
: APPLICANT: Carling, David			
: TITLE OF INVENTION: NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE			
: FILE REFERENCE: NGAP/PHM3758B/UST			
: CURRENT APPLICATION NUMBER: US/08/557, 006C			
: CURRENT FILING DATE: 1996-03-06			
: PRIOR APPLICATION NUMBER: PCT/G994/01093			
: PRIOR FILING DATE: 1994-05-20			
: PRIOR APPLICATION NUMBER: GB 9310489.1			
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: PRIOR FILING DATE: 1993-08-31			
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: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: cdna of rat
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US-08-357-006C-24

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 ; Patent No. 6124125
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 ; APPLICANT: Dartmouth College, St. Vincents Institute of
 ; APPLICANT: Medical Research, Kemp et al.
 ; TITLE OF INVENTION: No. 6124125el AMP Activated Protein Kinase
 ; NUMBER OF SEQUENCES: 64
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Jane Massey Licata, Esq.
 ; STREET: 66 E. Main Street
 ; CITY: Marlton
 ; STATE: NJ
 ; COUNTRY: USA
 ; ZIP: 08053
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
 ; COMPUTER: IBM PC
 ; OPERATING SYSTEM: WINDOWS 95
 ; SOFTWARE: WORDPERFECT 6.0 FOR WINDOWS
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/101.146
 ; FILING DATE: October 7, 1998
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PN7450
 ; FILING DATE: 8 JAN 1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jane Massey Licata
 ; REGISTRATION NUMBER: 32,257
 ; REFERENCE/DOCKET NUMBER: DC-0050
 ; TELEPHONE: (856) 810-1515
 ; TELEFAX: (856) 810-1454
 ; INFORMATION FOR SEQ ID NO: 44:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1647

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; TYPE: Nucleic acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: No
US-09-101-146-44

Query Match
Best Local Similarity 54.1%; Pred. No. 2e-31;
Matches 433; Conservative 0; Mismatches 365; Indels 3; Gaps 2;

Oy 158 gggccagagtcagggccagcagaagctccctccgggtgggttltacagacatcagcgag 217
Db 3 GGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 62
Oy 218 cctgggcaaaagcgaacttcgcggtgagagagagagagagagagagagagagagagag 277
Db 63 GCTGGCGCTCGGACCTTCGGGAAAGTGAGAGTGAGAGAGAGAGAGAGAGAGAGAGAG 122
Oy 278 ggttcaataaataatgtga-taaacagattagattcaagcaat--tggagaaat 334
Db 123 AGTTGCTGGAAGATACCTCAACCGGAGAGATTGGAAGCTTGAGCTGCTGGGAGAAAT 182
Oy 335 ctatcgtgaggttcagctgagatgagagagagagagagagagagagagagagagagag 394
Db 183 CCGCAGAGAGAGATCCAGAACCTGAACCTTTTCAGGACCCCTCATATATCAAACTGTACCA 242
Oy 395 ggtatggaacaaagagagagagagagagagagagagagagagagagagagagagag 454
Db 243 GGTCAATCAGTACACCGCTGTGATATTTTCATGCTCATGGAATATGCTCAGAGAGAGACT 302
Oy 455 gttgatatttgaacttccaaagagagagagagagagagagagagagagagagagagagag 514
Db 303 ATTGATTTATATCTGTAAATAATGAGAGTGTGACCAAAAGAGAGAGAGAGAGAGAGAG 362
Oy 515 gcaaatccctgcgcgtgagagagagagagagagagagagagagagagagagagagagag 574
Db 363 GCAGATCCTTCTGTGAGTGTGAGACTATTGTCACAGAGCATGTGTGTGTCACAGAGATTGAA 422
Oy 575 gaccgagagagagagagagagagagagagagagagagagagagagagagagagagagag 634
Db 423 ACCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 482
Oy 635 gaatttcaacagagagagagagagagagagagagagagagagagagagagagagagagag 694
Db 483 AAACATGATGTACAGATGTGTGAATTTTAAAGAACAGAGCTGTGTGCTGCCAATTTATGCTGC 542
Oy 695 cccggaagcttctgagagagagagagagagagagagagagagagagagagagagagagag 754
Db 543 ACCAGAGAGTAAATTCAGAGAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 602
Oy 755 cgtggtgctgagagagagagagagagagagagagagagagagagagagagagagagagag 814
Db 603 GGTCAATCTCTATCTCTGCTGTGTGAGAACTCTCTCTTTTATATGATATGACCAAGTGCAC 662
Oy 815 gctgagagagagagagagagagagagagagagagagagagagagagagagagagagagag 874
Db 663 TCTTTTAAAGAGATGTGTGAGAGAGATTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAG 722
Oy 875 tgaagagagagagagagagagagagagagagagagagagagagagagagagagagagag 934
Db 723 AATAAGCCTTTTGAAGCATATGTCGAGAGAGATCTATGAAAGAGGCGCACAAATAAAGA 782
Oy 935 gatccgagagagagagagagagagagagagagagagagagagagagagagagagagag 955
Db 783 TATCAGGAGACATGATGATT 803

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RESULT 6
 US-08-557-006C-44
 ; Sequence 44, Application US/08557006C
 ; Patent No. 6258547
 ; GENERAL INFORMATION:

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QY	278	ggttgacaataaataatgtga---	aaacagattagttcaaggcaatttggagaaat	3
Db	124	gttgcaatttaaatcttaataatgacgaagaatctgcagttatagatgttcttggaaaat	1	
QY	335	ctatcgtatgagttcagctctgtatgaagcttcttgaaaccaatcacacatcaaaagctttca	3	
Db	184	aaaacgagaaattcaaaaattcaaatcaactcttcttcgtatccatcatattcaaacatacca	2	
QY	395	ggttatgtgaacaagaagacatgccttthaatctgcatactaatcttcttaaaaatgggaaat	45	
Db	244	tgatcatagacattcccaacagatttttttatgtatgaatgaaatagtctctggagtgaaat	30	
QY	455	gttgattatttgaacttccaaacggagcaactgafgaaagaagcgcggaagaagtctcg	51	
Db	304	atttgactatacatctgtaaagcatgagcgggttgaaagatgaaagcaggcggctcttca	36	
QY	515	gcaaatcctgttcggcgtcggtggagtaacttcaagacatcatcatgcttcaacggagactcaa	57	
Db	364	gcaagattcgtctgctgtgtgataatcttcataaggacatagtgtgtctatccagagactgaa	422	
QY	575	gaccgaacacctctcgtctgtatgagcaacatgagacatcaagcggagaaatttgatttgg	634	
Db	424	accagagagatgcctctgtgatgtacaacatgaatgccaagcagaagcggattcttgattatc	483	
QY	635	gaatttcaacagtcaggaaagacctctgtccacgctggtgtgtggagcccccgatttcgcg	694	
Db	484	taatatatgtatcgatagtgtaattttctcttggaactatgcttgcgatacttcaaatatgagc	543	
QY	695	cccggaagcttttgaggggaagagatgatagaagccccacagcttgacaactcggagctctgg	754	
Db	544	acctggaatcatcatcctacagaaatctgatacgagctcgtgaagttgatatctcgagcgtcg	603	
QY	755	cgtggcgctgatacgtctgcgtctgcgtctctctcccttcgatacgggccccaaactcgcagc	814	
Db	604	tgatatcttgatactctctctcttcttggcaacctccaaattgatagagacatgatactaac	663	
QY	815	gctcgagacagcggtgtcgtcggagggccgcttcgcgaatccctcttcaatgtctcaagactg	874	
Db	664	gttatattagaagaatccgaggggtgtcctttataccagaatctcnaatctgtctgt	723	
QY	875	tgaagacctgtatccgcgatactcgtgtgtgtgagaccccgacagcgcatcacatcagccca	934	
Db	724	cgcacatctctctgtatgatactgtcgaagttgaaacacatgaaacgagaaactatcaaga	783	
QY	935	gatacggacagacacgggtgatt	955	
Db	784	catagaagagcatgaaatgatt	804	

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RESULT      9
US-09-212-771-1
; Sequence 1, Application US/09212771
; Patent No. 5958773
GENERAL INFORMATION
APPLICANT: Brett P. Monla
APPLICANT: Lex M. Cowser
TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-1 EXPRESSION
FILE REFERENCE: RTS-0034
CURRENT APPLICATION NUMBER: US/09/212,771
CURRENT FILING DATE: 1998-12-16
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 1
LENGTH: 2610
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (199)..(1641)
US-09-212-771-1

Query Match      3.9%; Score 102; DB 2; Length 2610;
Best Local Similarity 50.6%; Pred. No. 1,2e-12;

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Matches 355; Conservative 0; Mismatches 335; Indels 12; Gaps 4;
QY 219 ctgggcaaaagcaactctgcggtggtgaagctgcgcgcgacatcgaccacaaacgacg 278
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Db 664 ctgggcaaaagcaactctgcgcaaggtgatctctgtggaaggaagccacagccgctac 723
QY 279 gtgcgaataaataatgtataaacaagatagatcaa---gcaatttggagaaaatc 335
      ||||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 724 taagcatalgaagatccccaagaaggaagatcatctgtgcgaaggaaggtggtccacaca 783
QY 336 tatcgtgaaggttcagcgtgaagagctcttgaaacatcacacatcataaagctttaccag 395
      ||||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 784 ctacacgagaacccgcgcgcgcgaactccagacaccccttccacagcccttgaagtac 843
QY 396 gtatagaaacaaagacatgcttaccatcgtactgaattgtctaaaaatggaagatg 455
      ||||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 844 tcttcacagaccacagacgcctctgtctgtcatgagtaagcacaacgggggagagctg 903
QY 456 ttgcattatttgaacttccaaagggacactgagtgagaacgagcggaagattctg 515
      ||||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 904 tcttcacacctgtccggggaacgtgtcttcacgaaggaacggccgcttctatgagct 963
QY 516 caaatctctgcgcgcgtggaagtactgtcac---gacatacatctgcacgggagactc 572
      ||||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 964 gaagatgtgtcaagcccttgactccctgcgactcggagaagaacgtgtgtaccggagactc 1023
QY 573 aagacggagaacactcctgtcgtgaatgacaatgtgacatacagcttgcagatlttgaatt 632
      ||||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 1024 aagcttgagaaactcatgtcgtgaacgaagcgacatlaagatacagacttccggctg 1083
QY 633 gggaatttcta---caagtaagagaagactctgtccacgtgtgttggaagcccccgtat 689
      ||||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 1084 tgcagaaggaaggaatcagaagacgtgtccacatgaagaccttltgcgcacacactgagtac 1143
QY 690 ggcgcgcgcggaagatcttcttgagggggaaggaatatagaagggccccaacgggacatctgagc 749
      ||||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 1144 ctggcccccgaaggtgtcgtggaagacaatgactac---ggcgtgtcagaatgactgtgagg 1200
QY 750 ctgggagctgtgtcgtacgtccctgcgtctcctccctcctcgaatgggactaactg 809
      ||||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 1201 ctgggctgtgtcatgtacgaagatgagtggtgcgtccgtccctctctacaacagagacat 1260
QY 810 ccgaagctgagaacagcggtgtcgtggaagggccgcttcgcacatccctctctcatgtctcaa 869
      ||||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 1261 gagaagaacttltgagctcatccatcgaatgaagaaatccgcttccgcgcagacgttgtgcc 1320
QY 870 gactgtgagaagcctgataccgcgcacatgtctgtgtgagcccc 911
      ||||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 1321 gaggccaagtcctgtcttcaagggtcgtctcaagaagaagacccc 1362

RESULT 10
US-09-091-058-1
; Sequence 1, Application US/09091058
; Patent No. 6054285
; GENERAL INFORMATION:
; APPLICANT: Hemmlings, Brian A.
; APPLICANT: Frech, Mathias
; TITLE OF INVENTION: Screening Method
; FILE REFERENCE: 4-20683/A/20684/PCN
; CURRENT APPLICATION NUMBER: US/09/091,058
; EARLIER FILING DATE: 1998-06-10
; EARLIER APPLICATION NUMBER: PCT/EP96/04814
; EARLIER FILING DATE: 1996-11-05
; EARLIER APPLICATION NUMBER: 9525703.6
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2610
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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; NAME/KEY: CDS
; LOCATION: (199)...(1641)
US-09-091-058-1
Query Match 3.98; Score 102; DB 3; Length 2610;
Best Local Similarly 50.68; Pred. No. 1,2e-12;
Matches 355; Conservative 0; Mismatches 335; Indels 12; Gaps 4;
QY 219 ctgggcaaaagcaactctgcggtggtgaagctgcgcgcgacatcgaccacaaacgacg 278
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Db 664 ctgggcaaaagcaactctgcgcaaggtgatctctgtggaaggaagccacagccgctac 723
QY 279 gtgcgaataaataatgtataaacaagatagatcaa---gcaatttggagaaaatc 335
      ||||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 724 taagcatalgaagatccccaagaaggaagatcatctgtgcgaaggaaggtggtccacaca 783
QY 336 tatcgtgaaggttcagcgtgaagagctcttgaaacatcacacatcataaagctttaccag 395
      ||||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 784 ctacacgagaacccgcgcgcgcgaactccagacaccccttccacagcccttgaagtac 843
QY 396 gtatagaaacaaagacatgcttaccatcgtactgaattgtctaaaaatggaagatg 455
      ||||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 844 tcttcacagaccacagacgcctctgtctgtcatgagtaagcacaacgggggagagctg 903
QY 456 ttgcattatttgaacttccaaagggacactgagtgagaacgagcggaagattctg 515
      ||||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 904 tcttcacacctgtccggggaacgtgtcttcacgaaggaacggccgcttctatgagct 963
QY 516 caaatctctgcgcgcgtggaagtactgtcac---gacatacatctgcacgggagactc 572
      ||||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 964 gaagatgtgtcaagcccttgactccctgcgactcggagaagaacgtgtgtaccggagactc 1023
QY 573 aagacggagaacactcctgtcgtgaatgacaatgtgacatacagcttgcagatlttgaatt 632
      ||||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 1024 aagcttgagaaactcatgtcgtgaacgaagcgacatlaagatacagacttccggctg 1083
QY 633 gggaatttcta---caagtaagagaagactctgtccacgtgtgttggaagcccccgtat 689
      ||||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 1084 tgcagaaggaaggaatcagaagacgtgtccacatgaagaccttltgcgcacacactgagtac 1143
QY 690 ggcgcgcgcggaagatcttcttgagggggaaggaatatagaagggccccaacgggacatctgagc 749
      ||||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 1144 ctggcccccgaaggtgtcgtggaagacaatgactac---ggcgtgtcagaatgactgtgagg 1200
QY 750 ctgggagctgtgtcgtacgtccctgcgtctcctccctcctcgaatgggactaactg 809
      ||||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 1201 ctgggctgtgtcatgtacgaagatgagtggtgcgtccgtccctctctacaacagagacat 1260
QY 810 ccgaagctgagaacagcggtgtcgtggaagggccgcttcgcacatccctctctcatgtctcaa 869
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Db 1261 gagaagaacttltgagctcatccatcgaatgaagaaatccgcttccgcgcagacgttgtgcc 1320
QY 870 gactgtgagaagcctgataccgcgcacatgtctgtgtgagcccc 911
      ||||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 1321 gaggccaagtcctgtcttcaagggtcgtctcaagaagaagacccc 1362

RESULT 11
US-09-256-465-1
; Sequence 1, Application US/09256465
; Patent No. 6043090
; GENERAL INFORMATION:
; APPLICANT: Hemmlings, Brian A.
; APPLICANT: Frech, Mathias
; TITLE OF INVENTION: Screening Method
; FILE REFERENCE: 4-20683/A/20684/PCN
; CURRENT APPLICATION NUMBER: US/09/091,058
; EARLIER FILING DATE: 1998-06-10
; EARLIER APPLICATION NUMBER: PCT/EP96/04814
; EARLIER FILING DATE: 1996-11-05
; EARLIER APPLICATION NUMBER: 9525703.6
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2610
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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OTHER INFORMATION: unknown
US-09-467-082-3

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Query Match      3.4%; Score 88.4; DB 4; Length 2549;
Best Local Similarity 47.5%; Pred. No. 8.8e-10;
Matches 365; Conservative 0; Mismatches 391; Indels 12; Gaps 3;

QY 177 cagaatccctccgggtgtgttttaacgacatcgagcgaccctggcacaagcgcaacttc 236
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Db 186 cagaacacagccgacctgtgatcagtttgaacgaatcaagaccctcgacggctccctc 245

QY 237 gcgggtgtgaagctggcgcgcgcatcgagtcacccaacgacggttgcataataatt 296
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 246 gggcggtgtgtgtgtgaacacagaagagccgggaaccactatgcattgaagatcctc 305

QY 297 gataaacacgatttag---attcaagcaatttggagaaatctatcgtgaagttcagctg 353
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Db 306 gacaaacagaaggtgtgtgaacttgaacgaatcgaaacacacccctgaatgaagaagcgc 365

QY 354 atgaagcttctgaaccatccacacatcaaaagcttaccaggtatcagaaacaagagac 413
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Db 366 ctgcaagctgtcaacttcctcctcgtcgaactcgagttctcctcaagagacaactca 425

QY 414 atgcttaactgctacgtacgtattgtttaaataatggagaagtgttgatttgaacttcc 473
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Db 426 aacttaacatggtcatgtgaatgagtcgtcccgcggggagatgttctcacactacggcgg 485

QY 474 aacggcaccttgatgagaacgagcgcggaagaagttctgcaaatcctgtcggcgtg 533
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Db 486 atcggaaggtcagtgagccccaatgccgtttctacgcgcccagatcgtlcttgacctlt 545

QY 534 gagtactgtacacatccatccatcgctccacgggacctcaagaccgaagacctcgtctg 593
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Db 546 gagtactgtacacatccatccatcgctccacgggacctcaagaccgaagacctcgtctcat 605

QY 594 gatggcacatlgacatcaaacgctgcagatlttgatttgggaattctacaagatcagaa 653
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Db 606 gaccagcaggtcactacatcagtgacagacttcggttcgccaagcgctgaag----- 659

QY 654 gagcctctgtccagctgtgtgtggagcccccgtatgcggccccgggaagcttltgaggg 713
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Db 660 ggcgcacatcgacactgtgtggcaaccccgtacactgtgccccctgagattatccctgagc 719

QY 714 aagagatgaaagcccccagctggacatctggaccttggcgctgtgtgtactcgtg 773
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Db 720 aaaggtctaaacaagagcc---gtggactgtgtggcccttgggttcttactatgaatcg 776

QY 774 gtctggtgtctctcccttcgatatggcctaacttgcgcagcgttgagacagcggtgctg 833
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Db 777 gccgctgtctacccgctcttcttcgcagaccagcccatccagatctatgaaagatcgtc 836

QY 834 gagggcgcgtctccgcatcccttctcatgttcaagaactgtgagacgtgatccgcgcgc 893
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Db 837 tctgtgaaagtgtccttcccttccacttcaagctcagctctgacttgaagacactgctgcggaac 896

QY 894 atgtctgtgtgtgaccccgccagcgcatcacacatcgcccagatccggg 941
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Search completed: March 22, 2002, 13:20:34
Job time: 8972 sec

[illegible][illegible]

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Oy	1235	gtcgcgtgcagtagccttgccttctcccgatgagtcacagctgcagcgagatgltccgcg	1314
Db	482	GCTCACTTCA---GCCCTTATTAATCCCTCCGATACCAACTGCACTGGAGGTTCCGG-	537
Oy	1315	ccgcgcccgtgtccccaagaagcctgtctgagca--cagccatcagttagaagccagaag	1373
Db	538	CACGATCCATTTCCCCACAGACGTTGCTGTGACACCAAGCTATACGCAGAGAGGCCAGGCAG	597
Oy	1374	ggcgcgagcctlagagagagagacaggaacgcagagagatccctgcgccacgacacgagccgcg	1433
Db	598	GTCCACGCTGGAGAGAGAAACAGGAGGTACAGAACCCCGTACCGGAAACACAGCGGG	657
Oy	1434	aggcaaacaccgcgcgagatctcacaccgcgtcttc	1469
Db	658	AGGCACACAAATAGCTGAAGATCTCCAGCCATTTC	693

RESUPP #	4
LOCUS	AK017789 2411 bp mRNA HTC 05-JUL-2001
DEFINITION	Mus musculus 8 days embryo cDNA, RIKEN full-length enriched library, clone:5730525022, full insert sequence.
ACCESSION	AK017789
VERSION	AK017789.1 GI:12657214
KEYWORDS	CAP trapper.
SOURCE	Mus musculus (strain:C57BL/6J) 8 days embryo cDNA to mRNA, clone_11b;RIKEN full-length enriched mouse cDNA library clone:5730525022.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 2411)
TITLE	Carninci,P. and Hayashizaki,Y.
JOURNAL	High-efficiency full-length cDNA cloning Methods In enzymology. 303, 19-44 (1999)
MEDLINE	99279253
PUBMED	10394636
REFERENCE	2 (bases 1 to 2411)
AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome research. 10 (10), 1617-1630 (2000)
MEDLINE	20499374
PUBMED	11042159
REFERENCE	3 (bases 1 to 2411)
AUTHORS	Shibata,K., Itoh,M., Aizawa,K., Nagaoke,S., Sasaki,N., Carninci,P., Kono,H., Akiyama,J., Nishit,K., Kitsuma,T., Tashiro,H., Itoh,M., Suni,N., Ishii,Y., Nakamura,S., Hazama,N., Nisime,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kasaiwaig,I.K., Fujiwaka,S., Inoue,K., Togawa,Y., Iwawa,M., Ohara,E., Matsuhiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsunaga,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome research. 10 (11), 1757-1771 (2000)
MEDLINE	20530913
PUBMED	11076661
REFERENCE	4 (bases 1 to 2411)
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409, 685-690 (2001)
REFERENCE	5 (bases 1 to 2411)
AUTHORS	Adachi,J.J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A., Arikawa,T., Carninci,P., Fukuda,S., Fukushiri,Y., Futuno,M., Hanaogaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hirooka,T., Horii,F., Imotani,K., Ishii,Y., Itoh,M., Iwawa,M., Kato,H., Kawai,J.,

Kojima, Y., Onono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sekai, C., Sekai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shingawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Takawa, A., Takahashi, F., Tejima, T., Toyota, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

TITLE	Direct Submission
JOURNAL	Submitted (10-JUL-2000) Yoshinide Hayashizaki, The Institute of

COMMENT Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

FEATURES	Location/Qualifiers
source	1. .2411

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/strain="C57BL/6J"
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/dev_stage="8 days embryo"
137. .1600

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RPGALSPMOANTFOAPYNLDAOGFTCAKNTSVSDOYINDEINOIIPEDGVAINDSDSE
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Query Match	12.8%	Score 325;	DB 12;	Length 2411;
Best Local Similarity	61.2%	Pred. No. 1.7e-36;		
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Db	65	ggaacacact	gtgagcttt	aaaaagccagct	gtgatgaagaaact	tgaaagattttccgg	124
QY	243	gaggttcgcgt	atgaactcttgaacat	ccaacatcataaagct	ttaccagttatg		302
Db	125	gaggttcagat	aatgaatgcgttttggc	atccacacatcat	atcagacttcaccaggtc	atg	184
QY	303	gaacaagaag	cattgcttaccat	cgtaattgtgtaaaaa	tgagaatgtt	gat	362
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QY	363	tattgaattc	caacggtgcacct	gagtgagagaagggcg	cgaaagaatttc	ggaagtc	422
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QY	423	ctgtgcgcgt	ggagtgactgtc	acagcatcatcat	cgctccacggagct	ccaagacgag	482
	305	gttcacagcgg	gtgtattttttgttc	atcgttcggaatatac	gtttcatctcgatttt	aaaaaacccaa	364

OY	483	aacccgcgcgtggatctgagaaacatgaaatcaagctcgcagaatttggatttggaaatttc	542
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OY	543	tacaagtcagagagagccctctgtccacgctgtgtgtgtggagccccccgtatgcgcgccggaa	602
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OY	603	gtcctttgaggggaaagagatagaaaggccccagcttgagacatctgaaaccttgggcgtgtgt	662
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OY	663	ctgtaagcgcgcgtgtcgtggtgtctctccctctgaatggacctaaaccgcgcgaagctaga	722
Db	545	CTTATGTGCTGGTGTGTGGCGCCCTGCGCTTGTATGTGGAGCAACATGCAAAATCTGGG	604
OY	723	cagcgggtgtctggagagggcgccttcgcgatccccctcttcattgtctcaagactgtgaagc	782
Db	605	GCCCGCGTGAAGTGGGCAAGTTCCGCACTCCCGTTCTTTATGTCCACAGAGTGTGAGCAC	664
OY	783	ctgatacgcgcgaatgtctgtgtgtgtgaaccgcgcagcgcataaccatcgcgcagatccgg	842
Db	665	TTGATCCCCCACAATGCTGTGTGTAGATCCAAATTAAGCGCCTCTCAATGAAGACAGATCTGC	724
OY	843	cagacccggttgatgt-----cgagctgaagcccgcttgcgcggaaccgcgcgtccccgcc	896
Db	725	AGGCACAAGTGAATGAAGCTCGGAGATGACAGACCCCAACTTTTGACAGGTTAATAGCCGAG	784
OY	897	tctctcgacacacagctacaccttcaacctcaacctgtgcgactacgatgtgacgcgccttggatc	956
Db	785	TGCCAGCAACTGAAGGAAGAAAGGCAGTCCGAGACCCCTCAACGATGATGTCTCTTGGCT	844
OY	957	atgcagaccccttggcgttggacccgcgcagagagacggttgaagtcaacttgcataaacagcagctat	1016
Db	845	ATGGAAGACAATGGGGCTGGACAAAGAGGCGCACACTTCAAGTCATTAAAGTCAGATGCCTAT	904
OY	1017	aaccacttgtgtccatttatctactctctctcttgaagcgcgtcacaagagat	1067
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RESULT	5
BE247296	
LOCUS	
DEFINITION	BE247296 315 bp mRNA EST 15-NOV-2000 TCBAPLE4075 pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4075, mRNA sequence.

ACCESSION	BE247296	
VERSION	BE247296.1	GI:9099050
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	

REFERENCE	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo. 1 (bases 1 to 315)
AUTHORS	Wei, Y., Tsang, Y.T.M., Mei, G., Ku, J.M., Al-Osman Jr., F.R., Muzny, N., Bouck, J., Leukemia, R.A. and Margolin, J.F.
TITLE	Pediatric Leukemia cDNA Sequencing Project
JOURNAL	Unpublished (2000)
COMMENT	Contact: Dr. Judith F. Margolin

Texas Children's Cancer Center and Human Genome Sequencing Center
 at Baylor College of Medicine
 1102 Bates, MC3-3320 Houston, TX 77030, USA
 Tel: 832-824-4536
 Fax: 832-825-4038
 Email: clones@ccc.org
 Seq primer: M13 primer.
 Location/Qualifiers
 1. .315
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
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 /clone_id="Pediatric pre-B cell acute lymphoblastic

ACCESSION	BPF34711	mRNA sequence.
VERSION	BPF34711.1	GI:11622074
KEYWORDS	EST.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	NIH-MGC http://mgc.nci.nih.gov/.	
AUTHORS	1 (bases 1 to 646)	
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)	
JOURNAL	Unpublished (1999)	
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cga@bbs-remail.nih.gov Tissue Procurement: Jeffrey E. Green, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.llnl.gov Plate: LHAM9510 row: p column: 10 High quality sequence step: 646.	
FEATURES	Location/Qualifiers	
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	/clone_1kb="NCI_CGAP_SG2"	
	/lab_host="DH10B (TI phage-resistant)"	
	/note="Organ: salivary gland; Vector: pcMV-SPORT6; Site:1; NotI; Site:2; SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."	
BASE COUNT	172 a 153 c 178 g 143 t	
ORIGIN		
Query Match	11.1%; Score 280.8; DB 11; Length 646;	
Best Local Similarity	67.6%; Pred. NO. 4.1e-30;	
Matches 438:	Conservative 0; Mismatches 207; Indels 3; Gaps 3;	
G	gccagcagaagccctccggtcggttlttcacatcatcgagcggacccttgycacaagca	132
D	1 GGGGGTCGATGGCCCTCGCATCGGTACTAGCAATCACCAGCACACATCGGCAAGGCA	60
O	acttcgcggtgttgtagatcgcgcgcgcatcgagtccaaccaacgcgaagttgcaataaaa	192
D	61 ACTTGCGTGTGTTCAAGCGGCCGACGACACTTGTCACCAAGGCCAAGTTCATTAAAA	120
O	taattgataaaacacgatagattcaagaatttggagaa-aatcatcgtaggttcag	251
D	121 TCATAGATTAAGGCCAGCATGGAAGAAACCTTAAGAAGATGTGTCGGGAGGTTGAG	180
O	cftgataagcttcgaaacctcacacatcacataaagctttaccaggtltagaacaag	311
D	181 ATATGATGAGATGCT-TGCCATCCACATCATCATCAACTTACCAGGTCTGAGACAGG	239
O	gacatcgtttaatcgtcactgaatttgcataaaaaatggagaaatgtttgatatttgact	371
D	240 CCGCATGATTACTCGTGTGACAGATAACGCTACGGAGGGGAGATATTGTGACCACTTGTA	299
O	tccaacgggacacctgagttagaagaagaggcggaagaagttcttcgcaaatcctctcgccc	431
D	300 GCCCATGGAAGATGGACAAGGAAGAGCTCCACGGAATTTTAAACAGATCTCACACGG	359
O	gtcgagactgacacagaccatcacatcgctccacccggagacctaacagacagagacctctg	491
D	360 GTGATTTTTTGTGACCTGTCGGAATATCGTTACCTGATTTAAAACGCAAACTTACTT	419
O	ctgtagtcacaatcagatcgaactcgaacttggatattggaaatttctacaaagta	551

Db	420	CTGAGCGCCAAATCTGAATATCAAAATAGACAGACTTTGGCTTCAGCAACACTTCTACTCA	479
OY	552	ggaagagcctctgtccagtggtgtfgyggaagcccccgatagtcgcgcgccgggaagtccttgag	611
Db	480	GG-CAGATGCTTGAGAGCACGTGGTGTTGGCGCCCTCCATATGCCGCCCCAGAGCCTTTTGAA	538
OY	612	gggaagagtgctgaagagccccagctggaacacctggaagccctgggcctggtgctgtagctc	672
Db	539	GCGAAGGAATATGAGTGGGCCCAAAAGTGACATATGAGAGCCTTGGAGTGTCTCTATGTG	598
OY	672	ctggtctgaggttctctcccttcgattgagctaacctgcgcgaagctcg	719
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LOCUS	AI466101	439 bp	mRNA	EST	09-MAR-1999
DEFINITION	v40h03.y1 Soares_mammary_gland_NbMNG Mus musculus cDNA clone				
IMAGE	1246325.5' similar to SW:MSK_MOUSE_Q60670 PUTATIVE				
VERSION	SERINE/THEONINE-PROTEIN KINASE MSK ;, mRNA sequence.				
KEYWORDS	AI466101				
SOURCE	Mus musculus				
ORGANISM	house mouse.				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 439)				
TITLE	NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap .				
COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index				
JOURNAL	Unpublished (1997)				
CONTACT	Contact: Robert Strusberg, Ph.D.				
EMAIL	Email: cgapds-remail.nih.gov				
NOTE	This clone is available royalty-free through LNL ; contact the IMAGE Consortium (infoimage.llnl.gov) for further information.				
GI	GI:660013				
FEATURES	This read is a RESEQUENCE of a previously sequenced mouse clone				
FEATURES	This read has been verified (found to hit its original self in the				
FEATURES	correct orientation)				
FEATURES	Seq primer: -40RP from Glbco				
FEATURES	High quality sequence stop: 380.				
FEATURES	Location/Qualifiers				
FEATURES	1..439				
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FEATURES	/dev_stage="4 weeks"				
FEATURES	/lab_host="DH10B"				
FEATURES	/note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia				
FEATURES) with a modified polylinker; Site_1: Not I; Site_2: Eco				
FEATURES	RI; 1st strand cDNA was primed with a Not I - Oligo(dT)				
FEATURES	primer [5',				
FEATURES	TGTACCAATGTGAAGTGGCGCGCGCAAGCTTTTTTTTTTTTTTTTTTTTTT				
FEATURES	T 3]); double-stranded cDNA was ligated to Eco RI				
FEATURES	adaptors (Pharmacia), digested with Not I and cloned into				
FEATURES	the Not I and Eco RI sites of the modified pT7T3 vector.				
FEATURES	RNA provided by Dr. Minoru Ko, Wayne State Univ. Library				
FEATURES	constructed and normalized by Bento Soares and M. Felina				
FEATURES	Bonaldi."				
BASE COUNT	87 a	157 c	107 g	88 t	
ORIGIN					
Query Match	10.8%	Score 273.8	DB 10	Length 439	
Best Local Similarity	78.3%	Pred. No. 4.4e-29			
Matches 342	Conservative	0	Mismatches 92	Indels 3	Gaps 1

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Db	5	CAGCTCCGAGCTCAGACCTCAGACGCTCGAGGTTCTTCAAGAAATTTCTCCGTGTGAC	64
QY	1170	cccttcgcagctcgcagctcgtcgtccgcgcagccgcagaccttgctgcagtcgcctccag	1229
Db	65	CGTTTCGGGCCCTCTCTGTGTGGCCACAGGCCCGCCAGCCTTGGCTCAGTCTGCTCGACG	124
QY	1230	gcgcagatgagctgtgtgagctccagagctcgcgtgcagtgagctgtcttcctccggtgat	1289
Db	125	GCTGAGATAGACTGTGATCTCCACAGCTCATTCTCA--GCCCTTAATTAATTCCTCCGTGAT	181
QY	1290	gccagctcgcagggagtgcttcggccgcgcgcggcgtccggtcccaagcagcgtcgtgagcaca	1349
Db	182	ACCAACTGAGTGGAGTGTTCGGGACCGCATCTCTCCACGACGATCTGCTGACACA	241
QY	1350	gccatcagtgagagagccagcagggccggagcctcagaagagagcagagacacgcagagag	1409
Db	242	GCTATCAGGAGAGAGGCGCAGGAGGCTCCACACCTATAGAGAGACAGAGAGTCCAGANA	301
QY	1410	tcctctcccaagcagcagcggccggagcaacacctggccgaggtctccaccgcctctcc	1469
Db	302	CCCCGCCCCGGAAGCAGACGGCCGAGGCGACACATTGGCGAAGTCTCCACCATTTCTCC	361
QY	1470	ccacccacgcggccatgatatagctctccctccacacagcagcaagctctgagagagga	1529
Db	362	CGGCTACACCTCTTGCTAATTAATGCTCTCTCTGCGACGCGAGTCTCTCGAAGG	421
QY	1530	accagctcgtcagcttg	1546
Db	422	ACCAGCTCCGACAGCTG	438
RESULT	9		
LOCUS	AV612708	586 bp	MRNA
DEFINITION	AV612708 Bos taurus lung fetus Bos taurus cDNA clone E11D047B05 5'	EST	30-AUG-2000
ACCESSION	AV612708		
VERSION	AV612708.1	GI:9748378	
KEYWORDS	EST.		
SOURCE	cow.		
ORGANISM	Bos taurus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
	Bovinae; Bos.		
	1 (bases 1 to 586)		
	Sugimoto, Y., Hirotsune, S., Takasuga, A., Itoh, R., Jitohzono, A. and		
	Suzuki, H.		
TITLE	bovine cDNA sequencing		
JOURNAL	unpublished (2000)		
COMMENT	Contact: Yoshikazu Sugimoto		
	Animal Genetics Division		
	Shirakawa Institute of Animal Genetics		
	Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan		
	Tel: 81-248-25-5641		
	Fax: 81-248-25-5725		
	Email: kazusugie@ocn.ocn.ne.jp		
FEATURES	Single pass sequencing		
SOURCE	This clone was obtained from a polyA-deleted cDNA library.		
	Location/Qualifiers		
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	/dev_stage="fetus"		
	/lab_host="DH10B"		
	/note="vector: pZRL; site_1: SalI; site_2: NotI; poly A		
	was deleted from a NotI site"		
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ORIGIN			143 t

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Db	12	gctTTACCAGGTCATCGTAGACAGAACGGCATGATTATCTGTGTGACGAATATGTAAGTG	71			
OY	347	tggaggaatgttltgatatttgactccaaggagacctgtgtagaacccaggcgsgtaa	406			
Db	72	AGGGGAATATTATTGACCCACTGTGTGCCACCGCAGATGCAGAAAGAAGGAGGCCGTGC	131			
OY	407	gaagtctcygcaaaatcccgttcgcccgtgagtaactgltacagaccaatcacatcgtccacg	466			
Db	132	CAGGTCAACAACAGATCGTTTGACAGCCGTATTTTTGTACATGTGGAAACATTGTTCAATCG	191			
OY	467	ggaacctcaagaaccggaacacctcgtcgtgatatgtaacaatcgtacatacaagtctgcaattc	526			
Db	192	TGATTATAAAGCTGMAAATTTGCTCTCTCGACGCCCAATCTGAATATCAAGATAGCAGATTT	251			
OY	527	tggatttggagaattctctacaagtcaggagagccctctgcacagctgtgtgtggagcccccc	586			
Db	252	TGGCTTCAGTAACCTCTTACACCCCTGGGACAGCTACTGAAGACCTGTGTGGCAGCCCTTC	311			
OY	587	gtatgcgcccccggaagctctttagaagggaagagtatgaagagccccacgctggaacatctg	646			
Db	312	CTATGCTGCTCTCGAATCTTTGAAGGAAGAAGATATGACGAGCACCAAGGATGACATCTG	371			
OY	647	gagccttggcgttgtgtgcctgtacgtcctgtgtctctgcggtctctcccttcgatgtggcccaa	706			
Db	372	GAGCTCTGGAGATCGCTCTATGTCCTTGTGTGCGGGCCCCCTGCGCTTTGATGGGAGAC	431			
OY	707	cctgcgcgacgctggaacacgaggtgctgtgaaaggccgcctccgcacatccctctcatgtc	766			
Db	432	ACTGCAAGATCTGCGCGCGCCGGGTFTTAGTGAAGAAATTGGCATCCATTTTTATGTTC	491			
OY	767	tcaagactgtgaagagcctgtatccgcgcgacatgctgttgg-tggaccgccagagcgcatca	825			
Db	492	CACAGAAATGTAGAGCACTGATATCCGCCCAATGCGCTGTGTGGACCCCAACAGGCCCTCT	551			
OY	826	ccatcgcccaagatccgcgagcagcacggttgatg	857			
Db	552	TCATGAGACAGATCTGCAAGCCCACAGTGTGATG	583			
RESULT 10						
BE795309	763 bp	mRNA	EST	20-SEP-2000		
LOCUS	601586611F1 NIH_MGC_7	Homo sapiens cDNA clone IMAGE:3940970 5'				
DEFINITION	mRNA sequence.					
ACCESSION	BE795309					
VERSION	BE795309.1 GI:10216507					
KEYWORDS	EST.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.					
FILE	1 (bases 1 to 763)					
JOURNAL	NIH-MGC http://mhc.nci.nih.gov/.					
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1989) Contact: Robert Strausberg, Ph.D. Email: cgapbs-femail.nhl.gov Tissue Procurement: DCTD/DTP CDNA Library Preparation: Ling Hong/Rubin Laboratory Genomic Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: Image.lnl.gov Plate:LNCW/92 row: e column: 03 High quality sequence stop:551.					

FEATURES
source

FEATURES	SOURCE	Location/Qualifiers
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		/cell_line="MGC3"
		/lab_host="DH10B (phage-resistant)"
		/note="Organ: Lung; Vector: pOTB1; Site:1: XhoI; Site:2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(C). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT	226 a	162 c 189 g 186 t
ORIGIN		

Query Match	10.5%	Score 267	DB 11	Length 763
Best Local Similarity	61.1%	Pred. No. 3.1e-28		
Matches 449; Conservative	0	Mismatches 285;	Indels 1;	Gaps 1

QY	136	lccgclgttgtaaacctggtgcggagatcgaagtcacacaacacgagcttgcataaaaaaa	195
Db	1	TTGCCAAGGTGAAGTGGCCCGACACATCCTGACTGGGAAAGAGTAGCTGTGAAGATCA	60
QY	196	ttgataaaaccgatttgatccaagcaatttggsgaaaaatcactcgtaggttcaactga	255
Db	61	TTGACAAACATCAACTGAACTCTCCAGCCCTCCAGAAAATATTCCTGGGAAATAGAAATA	120
QY	256	tgaagctctgaaccatccacacaacataaagcttcaacggttatgtgaacaaagaca	315
Db	121	TGAAGCTTTGAATCATCTCCCAATAGTTAATTTATTGTAAGTATTTGAGACTAGAAAA	180
QY	316	tgctttacatcgttcaactgaaatttgctctaaatggagaatgtttgatatttgaactcca	375
Db	181	CGCTCTACCTGTTGATGAGTAGACCTAGTGGCGGAGAGGTATTTGATTACTTATGTGCTC	240
QY	376	acgagcaactctgtagagagacgagcgcggaagaagcttctgcaactctgtccgcccgtg	435
Db	241	ATGGCAGGATTAAGAAAGAAAAGGCTCGAGCCAAATTCGCCACATATGTCTCTGTGC	300
QY	436	agtaactgcacgacatcacatcgtlccacccggagacctcaagaccggaacctctgtctg	495
Db	301	AGTACTGTCCACCAAGATTATTTCTCATATAGACTTAAAGCAGAAAACCTGCTTTGG	360
QY	496	atggcaaatatgacatcaagctgtgcagatttggatttggaaatttctacaagtccagag	555
Db	361	ATGCTGATATCAACATCAAGATTCAGACTTTGGCTTCAGCAATGAAATCACTTTGGGA	420
QY	556	agacctctgccacgtgtgtgtggagccccccttatgcgcgccggaaagcttctgaagg-9	614
Db	421	ACAAGCTGGACACTTGTGTGGCAGTCCCTTATGCTGCCCCAGAACTCTTCCAGGGCA	480
QY	615	aaggaagatagaagccccccagctggaacatctgagacctgggctgtgtgtctgacgtctg	674
Db	481	AAAAAATTTGATGTGACCCGAGAGTGTGATGTGGAGCCTTAGAGATTATCTCTATACACTG	540
QY	675	gtctgcagcttctccccccttgatctgagggcctcaacctctgcagcgtctgagaacggcggtctg	734
Db	541	GTCAGCGGATCCCTGCTTTTGTATGACACAGAACTCAAGAGAGCTGCGGGAACGGGTACTG	600
QY	735	gaaggcgagcttgcgcatcccttcttcaatgtctcaagaactgttgagagcctgataccgcgcg	794
Db	601	AGGGGAAAATATACCTTATTCATCTTACATGTGCCAGGACGTGTGAAAACCTGTTAAGAA	660
QY	795	atgtcgtgtgtgtggaccccgccagcgcatcacatcgtccagatccggaacgcacgcgtgtg	854
Db	661	TTTCTCATCTTAAATCCAGCAAGAGGGCACTTTAAGCAAAATCATGAAGAATCGATGCG	720

QY	855	atgcgycctgagccc	865
Db	721	ATGAATGTGGTCCC	735

RESULT	11				
BE900808					
LOCUS	BE900808	677 bp	mRNA	EST	29-SEP-2000
DEFINITION	601674532p1 NIH_MGC_21	Homo sapiens	cdNA clone IMAGE:3957366	5'	
	mRNA sequence.				
ACCESSION	BE900808				
VERSION	BE900808.1	GI:10389353			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				

REFERENCE
1 (bases 1 to 677)
AUTHORS
NIH-MGC <http://mgc.ncl.nih.gov/>.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC).
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.

FEATURES

Location/Qualifiers
1. .677

```

//lab-most-1DH1UB (phage-resistant);
//note-1Organ: placenta; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAC(G). size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).

```

Query Match	10.5%	Score 265.4;	DB 11;	Length 677;
Best Local Similarity	62.1%;	Pred. No. 5.5e-28;		
Matches 419; Conservative	0;	Mismatches 256;	Indels 0;	Gaps 0;

OY	184	caataaaataatgatgaataaacgattagttctaaagcaatttgggaaatacatcg	24.3
Db	1	CAATAAATATATTTGACAAAACCTCAGTTGATCCACAGCTCTCMAAACTCTTCAGAG	60
OY	244	aggttcagctgtagaagcttcttgaccaatccacacataaagctttaccaggttat	303
Db	61	AAGTAGAGATATATGAGATTTTAAATATCCCAATATATGAGAACTTTTGGAATCTCATTTG	120
OY	304	aaacaaagacatgctttacatcgctcaactgaatttgcataaaatggaagaatggttcat	363.5
Db	121	AAACTGAAAAAACCTCTACTTATCATGTGAATATGCAAGTGGAGGTGAAGTATTTCAC	180
OY	364	attggaacttccaaagcggaaccttgtagaagaagagcgcggaagagttcttgcgaatcc	422.3
Db	181	ATTGTGTTGGCACAATGGCAGATGAGGAAAAAGAGCAAGATCTTAAATTTAGACAGATTG	240
OY	424	tttgcgcctgtgagtaactgtcaacgacacatcaatcgtctccacgcggagacctcaagaccaga	483

Db	241	TGTCGGAGTTCAATACTGGCATTAGAAAGGATCGTACACTGACAGACTTAAGGCTGAAA	300
QY	484	accctccgctgagatgycacaatgacatcaagctgpcagatlttggatlttggaaatttct	543.3
Db	301	ATCATTTGTTAGATGCGCGATATGAACTTTAAATATGACAGATTTTCGGTTTATGCATGCAAT	360
QY	544	acaaatcaggaaagacctctctccacgltgltgttggaaagcccccgatgcccgcgcgaag	603.3
Db	361	TTACTGTTGGGGGATTAACCTGACACAGCTTTGTGTGGCNACTCTCCATACGACGACACCTGAGC	420
QY	604	tctttgagggaaagaglatagaaagcccccaagctgacatctgagccttggcgtgtgtgc	663.3
Db	421	TCTTCCAGGCGCAAAATATGACGGGCGCAGAAAGGATGTGTGAGTCTGGGGTCAATT	480
QY	664	tgtacgtccctggtctgcggtctctctcccttcgatgtggcctaactgycgaagctgagac	723.3
Db	481	TATACACACTAGTCAATGAGGCTCACTTCCCTTCGATGGGCAAAACCTTAAAGAACTGAGAG	540
QY	724	agcggtggtcgtgaaagggccgtctccgatccctctctcatgltctcaagactgtgagaagc	783
Db	541	AGAAAGATATCAGAGGGCAATATCCGAAATTCCTTCAATGATGTACAGACTGTGAATAACC	600
QY	784	tgaatccgcgcgatgctgtgtgttggaaacccgcgcgcatcacacatctgcccagatccgc	843.3
Db	601	TTTCTCAAAACGTTTCTGTGCTGCTAAATCAATTAAACCGCGGCACTTATGAGCAATAATCATGA	660
QY	844	agcacgcgtgaaatgc	858
Db	661	AGGACAGGTGATCC	675

RESULT 12	LOCUS	DEFINITION
AI528387	435 bp	EST 18-MAR-1999
AI528387	u196f01.y1 Sugano mouse liver m1a Mus musculus cDNA clone IMAGE:1890289 5', mRNA sequence.	

ACCESSION	AI528387	
VERSION	AI528387.1	GI:4442522
KEYWORDS	EST.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	

REFERENCE
1 (bases 1 to 435)

AUTHORS
 Maritz, M., Hiller, L., Kucaba, T., Martin, J., Beck, C., Wyle, T., Underwood, R., Steptoe, M., Theising, B., Allen, M., Bowers, J., Pearson, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurr, R., Ritter, E., Kohn, S., Shih, T., Jackson, Y., Cardenas, M., McClann, R., Waterston, R. and Wilson, R.

TITLE	The Washu-NCI Mouse EST Project 1999
JOURNAL	Unpublished (1999)
COMMENT	Contact: Marra M/Washu-NCI Mouse EST Project 1999

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800
Fax: 314 286 1810

Fax: 314 286 1810
Email: monsooct@ustcn.ru.ac.cn

This clone is available royalty-free: mousses@cam.ac.uk

IMAGE Consortium (info@image.ljnl.gov) for further information.

MGI:974613

Seq primer: custom primer used
High quality sequence stop: 429.

FEATURES
SOURCE

1.435

/organism="Mus musculus"

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/strain="C57BL"
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/ab_xref="EAXon:10090"
/ab_cseq="TMACE.1990380#
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/clone IMAGE:1090203
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/c1onc_11b- cayanu mousec
/sex="female"
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/dev_stage="adult"
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/lab_host="DH10B"
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/note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII
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(CACTGCTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTGGCCCTACTGG], digested and cloned into distinct DraIII sites of the pM185-FL3 vector (5' site CACTGCTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCGCTCTTAAGACTGCG and 3' end primer CGACCTGAGCTGAGCA." 80 a 150 c 125 g 80 t

Query Match	10.3%	Score 261.6	DB 10	Length 435
Best Local Similarity	76.6%	Pred. No. 2.2e-27		
Matches 334	0	Mismatches 99	Indels 3	Gaps 1

QY 1492 tcgtctcccccacaccacgcagctctctgcagaggaaccagctctgcacagttgtctcga 1515

DB 2 TTGTCTCTCCCTCTGCCACGGGGGAGATCCCTCGGAAGGGACCACTCTCGACAGCTGCTTCC b1

QY 1552 cctctctgagcaaaagccccgcggtcagltgcaccccgcacactcaagggtctgc 1611

Db 62 CCTTCCTGCAAGTGAAGTCTGCAAGGCTTGGCAGTGGCCCTGGCCACCCGAGGGCTTC 121

QY 1612 cgggcgctcgtcccccgaagcgctgggcctcgcacctccatcgtgggctgcgacgtccgcacc 161

DB 122 TGGGCACGAGCTTCACATCGAGATTGGCCTTCCCTGGGATCACATCGACCAACC 181

QY 1672 cagtgcgcagcgtcagsgggccttggagagagctgtctcgtccctgtcagcttccagg 1731

DB 182 CTGTCTCCAGACTCAGCCAGGCTCTGGGCAACACCGCTTACCTCCCGTACGCTTCCAGG 241

Db 242 AGGACGGAGACGCTGATACCTCTCTACATCAGGGGCTGAAGCCCTTCGGGACAGC 301

QY 1792 tgagtagagaccacgcgagaccaaaggtttctgtagactgaacaaatcacaagggctgctc 185

DB 302 TGAGGAAAATGCGAGAGACCAAGGGTTCTTGGACTGACACAAGATCAAGGGTTGGTC 361

QY 1852 gccaggtgtgccaggtccctgcagccgggcagcagggggcgctgagcccttccag 1911

DB	362	GCCAGGTGTCCAG---TCCCTCCGTCGGAACTCCCGGGGAGGGATGAGTACTTTCACA	418
QY	1912	CCCGTGCACAGAGCCC	1927

Db 419 CCCAGCCCCAAGTC 434

RESULT 13
A0132239

LOCUS	866 bp	EST	24-OCT-2000
DEFINITION	AU132239 NT2RP3 Homo sapiens CDNA clone NT2RP3004052 5', mRNA sequence.		

ACCESSION	AU132239
VERSION	AU132239.1
KEYWORDS	GI:10992593 EST.

SOURCE	ORGANISM
human.	Homo sapiens
	Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi

REFERENCE
AUTHORS
Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 866)
Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,

TITLE Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
Isogai,T.
HRI human cDNA project

JOURNAL COMMENT
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory

Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
Email: genomese@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.

FEATURES

source
1. .866
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NT2RP3004052"
/clone_lib="NT2RP3"
/cell_type="teratocarcinoma"
/cell_line="NT2"
/note="Vector: pME18SF13; mRNA from NT2 neuronal precursor
cells after 2-weeks retinoic acid (RA) induction"
BASE COUNT 304 a 150 c 191 g 217 t 4 others
ORIGIN

Query Match 10.3%; Score 260.8; DB 10; Length 866;
Best Local Similarity 61.5%; Pred. No. 2.2e-27;
Matches 418; Conservative 0; Mismatches 262; Indels 0; Gaps 0;

Oy 188 aaaaataatgtataaacaagattagattcaagaatttgagaagaatcatcgtgagt 247
Db 1 AAAAAATATTGACAAACCTCACTTGAATCCACAAAGCTCTTCAGAGAAAGT 60
Oy 248 tcaagtgtgaagctctgaaacatccacatcaataaagcttaccagttatgaaac 307
Db 61 AAGATAATGAAGATTAAATCAATCCAAATAGTGAAGTATTCGAAGCATTTGAAAC 120
Oy 308 aaagaacatgcttcatcagctgactgaatttgctaaaatgagaagaattgattatt 367
Db 121 TGAATAAACACTCTACTATATCATGAAATATGCAAGTGGAGGTGAATTTGACTATT 180
Oy 368 gacttccaaagccacccagtgagtgagaagcgcggaagaagctctgcaaatctctc 427
Db 181 GGTTCACATGGCAGATGAAGAAAGAAAGAACAGATCTAATTTAGACATTTGTGTC 240
Oy 428 ggcggtgagtagtctgcaagcaccatcactcgtccacggagaccccaagccgagaact 487
Db 241 TGCAGTTCAATCTCCATTCAGAAACGGATCGTACATCGAGACCTCAAGGCTGAATAACT 300
Oy 488 cctgtgtatggaacatggaacatcaagctgcaattttgatttggaatttctacaa 547
Db 301 ATTGTAGATGCCATATGAAACATTAAATATGACAGATTTGGTTTACCAATGAATTTAC 360
Oy 548 gtcaagagagcctctgtccacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 607
Db 361 TGTGGCGGTAACCTCGACAGCTTTTGTGGCAGTCTCTCATTCGACACCTGACTCTT 420
Oy 608 tgaaggagaagagatgaagagcccccagctgagacatctggaagcctggcggtgtgtcta 667
Db 421 CCAGGCGCAAAATATGACGGGCCAGAAAGTGATGTGTGAGTCTGGGGGCTCAATTTATA 480
Oy 668 cgtcgt 727
Db 481 CACACTAGTCAGTGGCTCACTTCCCTTTGATGGGCAAAACCTTAAGAACTGAGAGAG 540
Oy 728 gt 787
Db 541 AGTATTAGAGGGAATATACAGATTTCTCTTACATGTCTACAGACTGTGAAAACCTTCT 600
Oy 788 ccgcgcgaatgt 847
Db 601 CAAAGCTTTCCGTGTGTAAATCAATTAACGGCGGACACTAGAGCAATATCATGACAGA 660
Oy 848 ccggt 867
Db 1 ||||| || ||

Db 661 CAGGTGATCATGCGAGGC 680

RESULT 14
LOCUS B6825423 748 bp mRNA EST 22-MAY-2001
DEFINITION 602746835F2 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:489824 5',
ACCESSION B6825423
VERSION B6825423.1 GI:14173010
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 748)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
COMMENT Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Plate: LNCM1792 row: e column: 09
High quality sequence stop: 746.

FEATURES

source
1. .748
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:489824"
/clone_lib="NIH-MGC_17"
/tissue_type="Thadomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: muscle; Vector: pORF7; Site:1; EcoRI;
Site:2: XhoI; cDNA made by oligo-dT priming.
directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT 222 a 163 c 182 g 181 t
ORIGIN

Query Match 10.2%; Score 257.4; DB 11; Length 748;
Best Local Similarity 61.3%; Pred. No. 6.8e-27;
Matches 448; Conservative 0; Mismatches 281; Indels 2; Gaps 2;

Oy 116 gacctgtggaagaagcaacttcggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 175
Db 14 GACCAATTGGCAAGGCTAATTTTGGCAAGTGAAGTGGCCCGACACATCCGACTGGGAA 73
Oy 176 gcaggttgcaataaataattgataaacaacgatttagatccaagaatttgagaanaat 235
Db 74 AGAGGTACTGTGAAGATCATTTGACAAAGCTCAACTGACTCTCTCCACCTCCAGAACT 133
Oy 236 ctatcgtgaagttcagctgtagaagctctgaacatcacacatcatalaagaatttaca 295
Db 134 ATTCCGCAAGTAAGAAATATGAAGGTTTGAATCATTCACCAACATAGTTAATTATTTGA 193
Oy 296 gttatggaacaagaacatgcttaccatcgtcaactgtaattgtctaaatgagaat 355
Db 194 AGTGATTGAGACTGAGAAAGCTCTACCTTGATGAGAGTACCTAGTGGCGAGAGGT 253
Oy 356 gttgatattttagcttcaacggcacttgagtgagaagcggcggaagaagttctgt 415
Db 254 ATTGATTACTAGTGGCTCATGCGAGATGAAGAAAAAGAGCGCTGAGCAAAATTCG 313

OY	416	gcaatccctgcgcgcctctgagctacttcaagaccatcacatcgttcaacgcggagacc	475
Db	314	CCAGATAGTGTCTGCTGTGCAGTACTGTCAACAGACTTTATTTGCCATGAGAGCTTAAA	373
OY	476	gaccgagaaacctctctgctgtagtagcaaatgagatcaaatcgtggcaatttggatttgg	535
Db	374	GGCAGAAAACTGCTCTTGATGCTGATATGAAATCATCAAGATTTGCACATTTGGCTTCAG	433
OY	536	gaattctacaaagtcagagagcctctgtccacgttgtgtggagccccccgtatgcgc	595
Db	434	CAATGAATTCACCTTTGGGAACAAGCTGGAAACCTTTGTGGCAGTCCCTTATGCTGC	493
OY	596	cccggaagctctttagg-9gaaagagatagaagccccacgcttgagatccttgagccctg	654
Db	494	CCCAAGACTCTTCCAGGGAAAAAATAATATGATGACCCGAGGTGAGATGTGTGAGGCTTAG	553
OY	655	gcgtgtgtcgttacctgtctgtgtcgtgctcctt-cccttcgatgtggcctaactgtcgcg	713
Db	554	GAGTTATCTCTTAACACTGCTGCAGCGGATCCCTGGGCTTTTGATGAGCAAGACCTTCAG	613
OY	714	agcgtgagaaacagcgggtgtcgtgaaagcgcgtctccgcgactccctctctcatgctcaagac	773
Db	614	GAGCTGCGGAAACGGTACTGAGGGGAAAAATACCCTATTTCATTCTTCAATGTCCACGGAC	673
OY	774	tgtagaagccttgatccgcgcgcatgtctgtgtgtgaaaccccgccagagcgcataccatcgc	833
Db	674	TGTGAAAACTGCTTAAGAAATTTCTATTCTTAAATCCAGCAAGAGAGGACACTTAAAG	733
OY	834	cagatcccgcca 844	
Db	734	CAAAATCATGAA 744	

	RESULT	15
	LOCUS	BFA70340
	DEFINITION	BF470340 393 bp mRNA EST 04-DEC-2000 UI-M-BH3-aux-c-08-o-II.r1 NH_BMAP_M.S4 Mus musculus cDNA clone
	ACCESSION	BF470340
	VERSION	BF470340.1 GI:11539523
	KEYWORDS	EST.
	SOURCE	house mouse.
	ORGANISM	Mus musculus
	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus
	AUTHORS	1 (bases 1 to 393) Bonaldi,M.F., Lennon,G. and Soares,M.B.
	TITLE	Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL MEDLINE COMMENT		Genome Res. 6 (9), 791-806 (1996)
	Contact:	Chin, H National Institute of Mental Health 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD 20892-9643, USA Tel.: 301 443 1706 Fax: 301 443 9890 Email: MEST@email.nih.gov
	CNA library Preparation:	M.B. Soares lab clone distribution: Researchers may obtain Bmap cdna clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of Bmap CDNs whose collaborative arrangements will be considered under appropriate and limited Seq primer: MJ3 Reverse.

FEATURES	Location/Qualifiers
source	1. .393

```

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-BH3-aux-C-08-0-UI"
/clone_1lb="NIH_BMAP_M_S4"

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`/dev_stage="-27-32 days"`
`/lab_host="DH10B (Life Technologies)"`
`/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NIH_BMAP_M_S4 library is a subtracted library of a series,
ultimately derived from a mixture of individually tagged
normalized libraries from ten regions of the mouse brain
(cerebellum, brain stems, olfactory bulbs, hypothalamus,
cortex, amygdala, basal ganglia, pineal gland, striatum,
hippocampus) after a series of subtractions to reduce the
representation of cDNAs from which ESTs had already been
generated. The following serially subtracted libraries
were generated in this process: NIH_BMAP_M_S4,
NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.1,
NIH_BMAP_M_S2, NIH_BMAP_M_S1. The subtracted library
(NIH_BMAP_M_S4) was constructed as follows: PCR amplified
cDNA inserts from NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and
NIH_BMAP_M_S3.1 clones from which 3' ESTs had been derived
was used as a driver in a hybridization with a pool of
the NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1
libraries in the form of single-stranded circles. The
remaining single-stranded circles (subtracted library)
was purified by hydroxyapatite column chromatography,
converted to double-stranded circles and electroporated
into DH10B bacteria (Life Technologies) to generate the
NIH_BMAP_M_S4 library. This procedure has been previously
described (Bonaldi, Lennon and Soares, Genome Research
6:791-806, 1996)".`

Query Match	Similarity	9.9%	Score 251	DB 11	Length 393
Best Local	Similarity	79.0%	Pred. No. 6	8e-26	
Matches	312	Conservative	0	Mismatches	80
				Indels	3
				Gaps	
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DB	2	CGAAGCTCAGACCTCAGCAGCTGAGGAGTCTCCAGAAATTCCTCCGHTGACCTTTC	61		
QY	1176	cgacctgccttgctgtgtcccgacgacgacagaccttggctgcaatcgtctccaaagcgag	12355		
DB	62	CGGGCTCTCTGCTGTGTCGCCACAGACCCCAAGCCCTTGGCTCACTGTCTCTCGAGGCTAG	121		
QY	1236	atggaactgtgagctccgaagactcgtctgacgttgccgtgtctctccggatgtagtcgaac	12950		
DB	122	ATAGACTGTGATCTCCACACTCACTTCA---CCCTTATTTATTCCTCCCTGGATACCAAC	178		
QY	1296	tgcagcggagatgtlctcggcccggcccgtgtcccaagcagcctctgtgaacagcactc	13555		
DB	179	TGCAGTGGAGTGTCCCGCACCCGATCATCTCCCCGAGAGTCTGTCGACACACTATTC	238		
QY	1356	agttaagaagaccgaagcgaagggcgccggcctctagaagaagacgaagaacgacgaagctccgt	1415		
DB	239	AGCGAGGGGGCCAGGAGGAGGTCCAGCTTAGAGAGGAACAGAGAGTCCAGGAACCCCTTG	298		
QY	1416	cccagcagcagcgggcgggaagacacaccttgcgcgaagttccacaccgacctctcccacat	1475		
DB	299	CCCGAAGACACAGGCCGGAAGGCACACATTGGCTGAAGTCTCCACCAATTTCTCCCGGTC	358		
QY	1476	acgcgcgcatagtatagtcgtctccctccacacac	1510		
DB	359	AACCTCTTGACATAATTTGCTCTCTCTCTCGGCAC	393		

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Job time: 5292 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 22, 2002, 10:51:02 ; Search time 89.2 Seconds
(without alignments)
6431.264 Million cell updates/sec

Title: US-09-787-559-1

Perfect score: 2533
Sequence: 1 ggcacccagcgcgcgcga.....aaaaaaaaaaaaaaaaaaaaa 2533

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgn2_6/ptodata/2/ina/PCUTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	285.4	11.3	2698	2 US-08-677-298-1	Sequence 1, Appli
2	203.2	8.0	2761	4 US-08-557-006C-24	Sequence 24, Appl
3	201	7.9	1742	4 US-08-557-006C-38	Sequence 38, Appl
4	201	7.9	2652	4 US-08-557-006C-39	Sequence 39, Appl
5	192.6	7.6	1647	3 US-09-101-146-44	Sequence 44, Appl
6	177.6	7.0	1747	4 US-08-557-006C-44	Sequence 44, Appl
7	177	7.0	1736	4 US-08-557-006C-37	Sequence 37, Appl
8	177	7.0	1783	4 US-08-557-006C-36	Sequence 36, Appl
9	102	4.0	2610	2 US-09-212-771-1	Sequence 1, Appli
10	102	4.0	2610	3 US-09-091-058-1	Sequence 1, Appli
11	99.6	3.9	1599	3 US-09-256-465-1	Sequence 1, Appli
12	98.2	3.9	1891	3 US-09-289-466-1	Sequence 1, Appli
13	96.6	3.8	1929	2 US-09-016-000-10	Sequence 10, Appl
14	95	3.8	1890	3 US-09-389-466-2	Sequence 2, Appli
15	88.4	3.5	2549	4 US-09-467-082-3	Sequence 3, Appli
16	87.2	3.4	4586	3 US-09-031-563-26	Sequence 26, Appl
17	87	3.4	2132	2 US-09-186-277-3	Sequence 3, Appli
18	86.8	3.4	1282	4 US-08-878-989-12	Sequence 12, Appl
19	86.8	3.4	1282	4 US-09-272-796-12	Sequence 12, Appl
20	86.8	3.4	1282	4 US-09-031-563-1	Sequence 1, Appli
21	83	3.3	4880	3 US-09-031-563-1	Sequence 1, Appli
22	83	3.3	5125	3 US-09-031-563-4	Sequence 4, Appli
23	83	3.3	5252	3 US-09-016-000-12	Sequence 12, Appl
24	82.4	3.3	2746	2 US-08-715-568A-2	Sequence 2, Appli
25	81.4	3.2	3471	2 US-09-159-385-4	Sequence 4, Appli
26	79	3.1	1429	2 US-09-186-277-4	Sequence 4, Appli
27	79	3.1	1429	4 US-09-186-277-4	Sequence 4, Appli

28	77.8	3.1	2770	2 US-08-878-989-8	Sequence 8, Appli
29	77.8	3.1	2770	4 US-09-272-796-8	Sequence 8, Appli
30	77.8	3.1	2789	3 US-09-136-282-3	Sequence 3, Appli
31	77.8	3.1	2789	4 US-09-505-744-3	Sequence 3, Appli
32	76.6	3.0	1637	2 US-08-966-316-10	Sequence 10, Appl
33	72.4	2.9	1761	4 US-08-924-183-3	Sequence 3, Appli
34	72.4	2.9	1761	4 US-09-488-364-3	Sequence 3, Appli
35	72.2	2.9	4162	2 US-08-459-448A-26	Sequence 26, Appl
36	72.2	2.9	4162	3 US-08-459-595A-26	Sequence 26, Appl
37	72.2	2.9	4162	3 US-08-459-504B-26	Sequence 26, Appl
38	72.2	2.9	4162	3 US-08-459-444-26	Sequence 26, Appl
39	72.2	2.9	4165	1 US-07-951-715A-26	Sequence 26, Appl
40	71.8	2.8	4935	2 US-08-631-097-3	Sequence 3, Appli
41	71.8	2.8	5886	4 US-08-810-712-9	Sequence 9, Appli
42	70.8	2.8	1821	4 US-09-522-800-15	Sequence 15, Appl
43	70.8	2.8	1821	4 US-09-522-800-17	Sequence 17, Appl
44	69	2.7	2783	3 US-09-136-282-1	Sequence 1, Appli
45	69	2.7	2783	4 US-09-505-744-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-677-298-1
; Sequence 1, Application US/08677298
; Patent No. 5863729
; GENERAL INFORMATION:
; APPLICANT: Pivnicka-Worms, Helen
; TITLE OF INVENTION: DNA SEQUENCES ENCODING HUMAN TCAK-1
; NUMBER OF INVENTION: KINASE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: USA
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/677,298
; FILING DATE: 09-JUL-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Caruthers, Jennie M.
; REGISTRATION NUMBER: 34,464
; REFERENCE/DOCKET NUMBER: 9-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2698 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: not relevant
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 376..2565
; US-08-677-298-1

Query Match 11.3%; Score 285.4; DB 2; Length 2698;
Best Local Similarity 61.3%; Pred. No. 2.9e-52;
Matches 460; Conservative 0; Mismatches 291; Indels 0;

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QY 117 accctggcaaaaggaacttcgcggtgggtgaagctggcgcgcatcgatccaccaaag 176
D 556 ACAATCGGCAAGGGGAAATTTTCAAAAGTAATTTGGCAAGACATATCTTACAGGACA 615
QY 177 caggttcgaataaataatgtataaacaacagatagatccaagaatttggaaatc 236
D 616 GAGGTTGCAATTAATAATATTCACAAACTCAGTTGAATCCCAAGTCTACAAAAGCTC 675
QY 237 tctcgtgaggttcagctgatgaagcttcgaaccatccacatcataaagctttaccg 296
D 676 TTCAGAGAAATAGATATATGAGATTTTAATCATCCCAATATATGTGATGATTTTCGA 735
QY 297 gttatgaaacaagaagacatgctttacatcgcactgaattgtcnaaaataggaaatg 356
D 736 GTCATTTGAACCTGAAAAAACTACTACTAATCATGATGATATGCAAGTGCAGTGAAGTA 795
QY 357 ttgattatttgactccaacgagcactgtagtgaagacgagcgcggaagaagttctg 416
D 796 TTTGACTATTTGGTTGCACATGGCAGATGAAGGAAAAAGAACGATCTAATTTTGA 855
QY 417 caatccgtcgcgcggtgagtagtctacgacatcacatcgctcccggaactcaag 476
D 856 CAGATTTGCTGCGAGTTCAATACTGCAATCGAAGGAGATGTCATCGAAGACCTCAG 915
QY 477 accgagaacctcctcgtgtagtgcacacatgacatcaagctgcagatttggattgg 536
D 916 GCTGAAATCTATGTTGTGATGCCGATATGAACATTAAATGCGAGATTTGGTTTAC 975
QY 537 aattctcaagatcagagagcctctgccacgtggtgtggaagcccccgatccgccc 596
D 976 AATGAATTTACTGTTGGCGGTAACACTGACACACGTTTGTGGCAGTCTCCATACACAGA 1035
QY 597 ccggaagctcttgaggaggaaagatgaagggcccgcccgatgacatcctggagcctgg 656
D 1036 CCTAGCTCTTCCAGGCGCAAGAAATATACGGGCCAGAAAGTGGATGTGTGGATCGGG 1095
QY 657 gtggtcgtacgtcctcgtcgtcgtctcctcccttcgaatggcctaaccctgcagag 716
D 1096 GTCAATTTATACACACTGAGTCAAGTGGCTACACTTCCCTTTGATGGGCAAAACCTAAAGGA 1155
QY 717 ctggaagcggggtgctggaagggccgcttcgcgaccccttcctatgtctaaagctgt 776
D 1156 CTGAGAGGAGAGATTTAAGAGGAAATACAAATTTCCCTTCTACATGCTACACACTGT 1215
QY 777 gagaagcctgacccgcgcatgctgtgtgtggaaccccgcaagcgcatcacatcgccag 836
D 1216 GAAAACTTCTCAAAAGTTTCTGCTGCTAATTCATTAATTAACCGCGCATCTTAGACGA 1275
QY 837 atccggcagcaccggtgtagtgcgggtgagc 867
D 1276 ATCATGAAGGACAGGTGATCATGTCAGGCG 1306

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; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 24
; LENGTH: 2761
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA of rat
; OTHER INFORMATION: Liver AMP protein kinase
US-08-557-006C-24

Query Match      8.0%; Score 203.2; DB 4; Length 2761;
Best Local Similarity 53.9%; Pred. No. 1.2e-34;
Matches 440; Conservative 0; Mismatches 373; Indels 3; Gaps 1;

QY 44 cagcgcgaccccgcgccgaagatgaagggccagcagaagcccccctcggtgtgtttaa 103
D 11 ccgcgcgcgaacatggtcgaagaagcagcagcgcggtgtgtgaagatcgcgacacta 70
QY 104 cgacatcgagcgagcccttgagcaaaagcacttcgcggtggtggaagctggcgcgcatcg 163
D 71 cgtgctggggagaccccttggcgctgcgcaccttcggaagtgaaatggaagacaatca 130
QY 164 agtccacaaacgcaggtgtgcaataaaataatgataaaacagat--agattcaag 220
D 131 attgacagggcatalaagtgtagcagtttaagatccttaaatagacgaagattcgcagttaga 190
QY 221 caatttggagaatctatcgtgtaggttcagctgtgaagctcttgcacatccacat 280
D 191 tgttltggaataaataaaacggaatctaaatccttgcactcttcactcctcatat 250
QY 281 cattaagcttaccaggttatgaaacaaagacatgcttcatcgtcactgaatttcg 340
D 251 tatcaaacctctacaaagtatcagcatctccacagacttlttaagtataagaaatgt 310
QY 341 taaaatggagaagaatgttgaattatgtgacttccaaacgggcaccttgatgaaacgagcg 400
D 311 gctcgtgagtgatgtgtcgtacatcatctgtaaacacggagaggtgtgaagaggttgaagc 370
QY 401 ggggaagaaggtctggaatccgttcgtgcgctgtagtgactcttcacgacatcacatcgt 460
D 371 tgcgcgctctccagcagatcttgcctgcgtgcgtgactctgtaacgaagcatatgttgt 430
QY 461 ccaccggagcctcaagacccgaacactcctcgtgtgaatgacaacatgacatcaagctggc 520
D 431 ccacagggccctgaagccagagacggtgtcgtgacgcccagatgaatgacaaagtagc 490
QY 521 agatttggatttgggaattctcaagtcagagagagcctctgtccacgtgtgtgtggag 580
D 491 tgaacttgcgactctctaataatgtlcaagatgtgaattctcagaaactagctgtgtgac 550
QY 581 cccccctgctgcgcgcgcgcgaagctcttgagggggaagagatgtgaagggccccaagctgga 640
D 551 gccaaattatgcagcagcgggaaggtcatctcaggaagagcgtcatgcggtcccgaggttga 610
QY 641 catctgagcctcggcggtgtgtgtgtgtagcgttcctgtgtcgtgtctcctcccttcgatg 700
D 611 tatctgagcgtgtgtgtatctcgtatcgtccttctccttctgtgcacccctccgttgaga 670
QY 701 gcctaacctgcgcagcgtgagacagcgggtgtctgtgaagggcgcgtccgcacatcccttct 760
D 671 tgagcagctgctcagcctctttaaagaagatccgaggggtgtgttctatcccgagta 730
QY 761 catgtctcaagactgttgagagccttatccgcgcatgctggtgtgtggaaccccgcaagg 820
D 731 tctcaaccgttctatctgcactctgtcatgacatgtcgcgaagtgtgaagccttgaagcg 790
QY 821 catcacatcgccagatccgcgacagcagcagcgtgagat 856
D 791 agcaactatcaaaagacatacagagagcatgaatgagct 826

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RESULT 3


```

Db 310 gttcactacatctgtaaacacgagaggttgaagagtgtgaagctcgccgctcttcca 369
Qy 416 gcaatcctgctcgccgtgagtagtactgtaacacatcacatcgctccacggagacctcaa 475
Db 370 ggaattctgctcgctgtagtactgtaacacatcacatcgctccacggagacctcaa 429
Qy 476 gaccgagaaacccctgctgtagtactgtaacacatcacatcgctccacggagacctcaa 535
Db 430 gcaatcctgctcgccgtgagtagtactgtaacacatcacatcgctccacggagacctcaa 489
Qy 536 gatttctcaacgagtagagagagctctgctcagctgtgtgtgagagcccccgatgcccgc 595
Db 490 taatatgtagtcaagtagtgaattcttaagaactagctgtgtagtccgaataatgcaagc 549
Qy 556 cccggaagctcttgaagggaagtagatgaaggccccacgctgtagatctgtagagctggg 655
Db 550 accgagagctacatcagagaagagctgtagtgcgctcctgagagctgtagatctgtagagc 609
Qy 656 cgtgtgtgtgtagtgcgctcctgctcctgctcctcctcctcctcctcctcctcctcctc 715
Db 610 tgtatccgtatgctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 669
Qy 716 gctgtagacagcggtgtgtgagagcgctcctcctcctcctcctcctcctcctcctcctc 775
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Qy 776 tgaagacccgtagcccgtagtctgtgtgtgtagaccgccgaaggcagatcacatcgccca 835
Db 730 tgcactctcgtatgtagatgtagtgcaggtgtagcccttgaagcgagcaatatacaaga 789
Qy 836 gatccgagcagccggtgat 856
Db 790 catagagagcatgtagt 810

```

RESULT 5

US-09-101-146-44
Sequence 44, Application US/09101146
Patent No. 6124125

GENERAL INFORMATION:

APPLICANT: Dartmouth College, St. Vincent's Institute of
APPLICANT: Medical Research, Kemp et al.
TITLE OF INVENTION: No. 6124125el AMP Activated Protein Kinase
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jane Massey Licata, Esq.
STREET: 66 E. Main Street
CITY: Marlton
STATE: NJ
COUNTRY: USA
ZIP: 08053

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PC
OPERATING SYSTEM: WINDOWS 95
SOFTWARE: WORDPERFECT 6.0 FOR WINDOWS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/101,146
FILING DATE: October 7, 1998
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PN7450
FILING DATE: 8 JAN 1996
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: DC-0050
TELECOMMUNICATION INFORMATION:
TELEPHONE: (856) 810-1515
TELEFAX: (856) 810-1454

INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 1647

```

; TYPE: Nucleic acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: NO
US-09-101-146-44

```

Query Match 7.6%; Score 192.6; DB 3; Length 1647;
Best Local Similarity 54.2%; Pred. No. 1.8e-32;
Matches 434; Conservative 0; Mismatches 364; Indels 3; Gaps 2;

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Qy 59 gggcagagctggagggccagagaagccccctccgggtggtttttagacatcgagcgagc 118
Db 3 gggcagagctggagggccagagaagccccctccgggtggtttttagacatcgagcgagc 62
Qy 119 ccttgagcaaaagcaattcgcggtgtgtagagctggtcgcgatcgagtcacaaagcga 178
Db 63 GCTGGGCGTGGGCGGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 122
Qy 179 gtttgcataaataaatgata-aaacagattagatccaagaatt--tggagaatat 235
Db 123 AGTTGCTGTGAAGATTAATCAACCGCAGAGATTCGAAGCTTGACGTGTCGGGAAAT 182
Qy 236 ctatcgtagagctcgtatgaagctctctgtagaaccatccacacataaagctttacca 295
Db 183 CCGCAGAGAGATCCAGAACCTGAGGCTTTCAAGGCGGCGGCGGCGGCGGCGGCGGCGG 242
Qy 296 gttatgagaacaagaagacatgcttctacatgctcagatgaattgtctaaataagggagaat 355
Db 243 GGTTCATCACTACACCGTCGTGATATTTTCATGTCATGATGATATGTCGAGGAGAGCT 302
Qy 356 gtttgaatttgaattccacagcgacccctgtagaagcagagcgcggaagaagttctg 415
Db 303 ATTTCATTAATCTGTAATAAATGGAAGTGTGAGCGAAGAAAGAGAGTGCAGCTGTCCA 362
Qy 416 gcaatcctgctcgccgtgagtagtactgtaacacatcacatcgctccacggagacctcaa 475
Db 363 GCAGATCCTTTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 422
Qy 476 gaccgagaaacccctcctgtagtagcaacatgtagacatcagctgtagatctgtagtgg 535
Db 423 ACCTGAAACGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 482
Qy 536 gaattctcaacgtagcagagagcctcctgtagcagctgtgtgtgagagcccccgtagtcgc 595
Db 483 AAACATGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 542
Qy 596 cccggaagctcttgaagggaagagtagatgaaggcccccaagctggaatctgtagagctgg 655
Db 543 ACCAGAAATTAATTCAGGAAGATTCACGACGACGACGACGACGACGACGACGACG 602
Qy 656 cgtgtgtgtgtagtgcctcctgtagtagcctcctcctcctcctcctcctcctcctcctc 715
Db 603 GGTCAATTCCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 662
Qy 716 gctgagacagcggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 775
Db 663 TCTTTTAAAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 722
Qy 776 tgaagacccgtagcgcgcatgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 835
Db 723 AATTAACCTTTTGAAGCATATGCTGAGGATGATGATGATGATGATGATGATGATGAT 782
Qy 836 gatccgagcagccggtgat 856
Db 783 TATCAGGAACATGATGATT 803

```

RESULT 6

US-08-557-006C-44
Sequence 44, Application US/08557006C
Patent No. 6258547
GENERAL INFORMATION:


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QY 416 gcaatcctctgcgcgttggagtaactgtcacgaccatcacatcgtccacgggacctaa 475
D 303 gcaagattctctgtctgtggaactgtcatagagcatatgttcttcacgaagacctgaa 422
QY 476 gaccagaaacctcctctgctggaagcaacatggaacatgaactcgtgcaagatttggatttg 535
D 423 accagagaaatgtcctctgtgtgatacacaatgaaatgaaatgaaatgaaatgaaatgaaat 482
QY 536 gaattctacaagtcaggaagagcctctgtccacgttggtgtggtggtggtggtggtggtggt 595
D 483 taatatgtatgtcagatgtgtgaattctcgaagactagttgtggtggtggtggtggtggtggt 542
QY 596 ccggaagcttcttgaagggtggaaggaatgaagagcccccacgtgacatctggaagcctgg 655
D 543 accggaagatctcctcaggaagcagatgtatgaggtcctcgaagctgataatctcggagctg 602
QY 656 cgtgtgtctgtaagctcgtctgctgctgtctctcctcctgagtggtggtggtggtggtggt 715
D 603 tgtatctgtatgtcctctctctctgtggaacccctccatctgagatgaaatgaaatgaaatg 662
QY 716 gctgagacagcgggtgtctggaagcgcctcgcacatccctctcctcctcctcctcctcctc 775
D 663 gttatttaagaagatccgaaggggtgtcttattatcccaagaaatccatccatcgtctctgt 722
QY 776 tgaagacctatccgcgcagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 835
D 723 cgcactctcctgtatgcatatgctgcaaggttgacccactgaaacaggaactatacaaga 782
QY 836 gatccgacagcaccggtgat 856
D 783 cataagagagcatgaatggt 803

RESULT 8
US-08-557-006C-36
; Sequence 36 Application US/08557/006C
; Patent No. 6258347
; GENERAL INFORMATION:
; APPLICANT: Berl, Rajinder K.
; APPLICANT: Carling, David
; APPLICANT: Forde, Robert A.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE
; FILE REFERENCE: NCAP/PHM3758/0ST
; CURRENT APPLICATION NUMBER: US/08/557.006C
; PRIOR FILING DATE: 1996-03-06
; PRIOR APPLICATION NUMBER: PCT/GB94/01093
; PRIOR FILING DATE: 1994-05-20
; PRIOR APPLICATION NUMBER: GB 9310489.1
; PRIOR FILING DATE: 1993-05-21
; PRIOR APPLICATION NUMBER: GB 9318010.7
; PRIOR FILING DATE: 1993-08-31
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 36
; LENGTH: 1783
; TYPE: DNA
; ORGANISM: Human AMP protein kinase
US-08-557-006C-36
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Query Match 7.0%; Score 177; DB 4; Length 1783;
Best Local Similarity 52.2%; Pred. No. 4.1e-29;
Matches 418; Conservative 0; Mismatches 380; Indels 3; Gaps 1;

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QY 59 gggccagagtcagagcagagagagagagagagagagagagagagagagagagagagagagag 118
D 4 ggtctgagagcagagagagagagagagagagagagagagagagagagagagagagagagagag 63
QY 119 ccttgagagagagagagagagagagagagagagagagagagagagagagagagagagagagag 178
D 64 gctgagagagagagagagagagagagagagagagagagagagagagagagagagagagagag 123
```

```
QY 179 ggttgcataaataaataatgata--aaacagatagattcaagcaatttgagaaat 225
D 124 agtgcagtttaaaatcttaataatgacagaaagatcgcagtttgatgtctgtgaaat 183
QY 236 ctatcgtgagaggttcaagctgtatgaagctcttgaacacatccacatcaataaagcttacc 295
D 184 aaacagagaaatctaaataatcaaacctctctgcatccatccatataatcaaacatacca 243
QY 296 ggtatgaaacaaagagacatgctttacatcgtcactgtaatttgcataaaatgagaaat 355
D 244 ggtgatacagaccccaacagatcttttatgtgaaatgagaaatggtctgtgaggtgaaat 303
QY 356 gttgattatctgaactccaacgggacacgtgaaatgaaacagagcggcggaagaagctg 415
D 304 attgcatcaatctgtaagatgagaggttgaagagatgaaagagcagagcgtcttca 363
QY 416 gcaaacctctgcgcgttgaagtaactgtacagacacatccatccatccatccatccatccat 475
D 364 gcaagatctgtcgtcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 423
QY 476 gaccagaaacctcctctgtgagacacacatggaacatgaagctggaagatttgatttg 535
D 424 accagagaaatgctcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 483
QY 536 gaattctacaagtcaggaagacccctctcgcacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 595
D 484 taatatgtatgataatgtgaaattcttgaagactagttgcatccatccatccatccatccat 543
QY 596 ccggaagctcttgaagagagagagagagagagagagagagagagagagagagagagagag 655
D 544 accggaagatcctcagagcagatgtatgacagaggtcctgaagttgatactcgtgagagctgt 603
QY 656 cgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 715
D 604 tgtatctgtatgtcctctctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 663
QY 716 gctgagacagcgggtgtctggaagcgcctcgcacatccctctcctcctcctcctcctcctc 775
D 664 gttatttaagaagatccgaaggggtgtcttattatcccaagaaatccatccatccatccat 723
QY 776 tgaagacctatccgcgcagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 835
D 724 cgcactctcctgtatgatalgtcgcaggttgacccactgaacagagcaactatcaaga 783
QY 836 gatccgacagcaccggtgat 856
D 784 cataagagagcatgaatggt 804
```

```
RESULT 9
US-09-212-771-1
; Sequence 1, Application US/09212771
; Patent No. 5958773
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-1 EXPRESSION
; FILE REFERENCE: RTS-0034
; CURRENT APPLICATION NUMBER: US/09/212,771
; CURRENT FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 2610
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (199)..(1641)
US-09-212-771-1
```

Query Match 4.0%; Score 102; DB 2; Length 2610;
Best Local Similarity 50.6%; Pred. No. 5.5e-13;

```
Matches 355; Conservative 0; Mismatches 335; Indels 12; Gaps 4;
QY 120 ctgggcaaaagcaactcgcgtgtgtgaagctggcgcgacatcagatccaccaaaacgag 179
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 664 ctgggcaaaagcaactcgcgtgtgtgaagctggcgcgacatcagatccaccaaaacgag 723
QY 180 gtgcgaataaataatgatgaacaacgattagattcaa---gcaattggagaanaatc 236
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 724 taagccatgaagatccccaagaaggaatcatcgttgcgaagacgaggtgcccacaca 783
QY 237 taatcgttaaggttcaagtgtaagcaatctctgaacatccacatcaaaacattaccag 296
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 784 ctacacggaacacgcgtctcgtcaaacatccacgaccccttccacagccctgaagtac 843
QY 297 gtatagaaacaaagacatgtcttacatcgtcaatctgaattgtctaaaatgtgagaatg 356
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 844 tcttccagaccacgacgcgcctctgtcttgcatagtgaatcgaacgagggcgagctg 903
QY 357 ttgcattatctgaacttccaaacgggacacctgagtgaagaacgagcgcggaagaattctg 416
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 904 tcttccacacctgtccgggaacgtgtgtctccgaagacggcgccgcttctaatgagct 963
QY 417 caaatcgtcgcgcgtggaagctgtctacac---gacatcaacatcgtccacgggaacctc 473
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 964 gaagtgtgtcagacccttggaactacatcgtcgtcgtgaagaagacgtgtgtacccggagctc 1023
QY 474 aagacgagaacatcctcgtcgtgaatgcaacatgacatcaacgtcgtcagatttgattt 533
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1024 aagctggagaacctcatgctggaacgaagacgagacatlaagatcaacagacttgggctg 1083
QY 534 ggggaatttcta---caagtacagaagagcctctgtcacaagtgtgttggagaccccgat 590
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1084 tgcagaagagaggaatcaagagacgtgtccacatgaagacatttgcgcacacccgtgaatc 1143
QY 591 gccgcgccgggaagctcttctggagggaagagtaagaagccccccacgagacatctgagc 650
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1144 ctggcccccgaggtgctggaggaacatgaactac---ggcggtcagtggaactgtgtgggg 1200
QY 651 ctgggctgtgtgtcgtacgtctgtcgtgtctcgtctccctcgtatggtggtcctaactg 710
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1201 ctgggctgtgtgtcgtacgtctgtcgtgtctcgtctccctcgtatggtggtcctaactg 1260
QY 711 ccgaagctgagacagcggtgtgtgtggaagcgccgtctccgacatcccttcttaattctcaa 770
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1261 gagaagcttcttgagctacatcctcatgtgagaagatccgcttcccgacagcttgttccc 1320
QY 771 gactgtgagagcgtgatccgcgcgatgtgtgtgtgagcccc 812
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1321 gaggccaaagctcctgtcttcaagggtgtctcaagaagaagacccc 1362

RESULT 10
US-09-091-058-1
; Sequence 1, Application US/09091058
; Patent No. 6054285
; GENERAL INFORMATION:
; APPLICANT: Hemmlings, Brian A.
; APPLICANT: Frech, Mathias
; TITLE OF INVENTION: Screening Method
; FILE REFERENCE: 4-20683/A/20684/PCT
; CURRENT APPLICATION NUMBER: US/09/091, 058
; EARLIER FILING DATE: 1998-06-10
; EARLIER APPLICATION NUMBER: PCT/EP96/04814
; EARLIER FILING DATE: 1996-11-05
; EARLIER APPLICATION NUMBER: 9525703.6
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2610
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
```

```
NAME/KEY: CDS
LOCATION: (199)..(1641)
US-09-091-058-1
Query Match 4.08; Score 102; DB 3; Length 2610;
Best Local Similarity 50.68; Pred. No. 5.5e-13;
Matches 355; Conservative 0; Mismatches 335; Indels 12; Gaps 4;
QY 120 ctgggcaaaagcaactcgcgtgtgtgaagctggcgcgacatcagatccaccaaaacgag 179
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 664 ctgggcaaaagcaactcgcgtgtgtgaagctggcgcgacatcagatccaccaaaacgag 723
QY 180 gtgcgaataaataatgatgaacaacgattagattcaa---gcaattggagaanaatc 236
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 724 taagccatgaagatccccaagaaggaatcatcgttgcgaagacgaggtgcccacaca 783
QY 237 taatcgttaaggttcaagtgtaagcaatctctgaacatccacatcaaaacattaccag 296
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 784 ctacacggaacacgcgtctcgtcaaacatccacgaccccttccacagccctgaagtac 843
QY 297 gtatagaaacaaagacatgtcttacatcgtcaatctgaattgtctaaaatgtgagaatg 356
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 844 tcttccagaccacgacgcgcctctgtcttgcatagtgaatcgaacgagggcgagctg 903
QY 357 ttgcattatctgaacttccaaacgggacacctgagtgaagaacgagcgcggaagaattctg 416
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 904 tcttccacacctgtccgggaacgtgtgtctccgaagacggcgccgcttctaatgagct 963
QY 417 caaatcgtcgcgcgtggaagctgtctacac---gacatcaacatcgtccacgggaacctc 473
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 964 gaagtgtgtcagacccttggaactacatcgtcgtcgtgaagaagacgtgtgtacccggagctc 1023
QY 474 aagacgagaacatcctcgtcgtgaatgcaacatgacatcaacgtcgtcagatttgattt 533
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1024 aagctggagaacctcatgctggaacgaagacgagacatlaagatcaacagacttgggctg 1083
QY 534 ggggaatttcta---caagtacagaagagcctctgtcacaagtgtgttggagaccccgat 590
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1084 tgcagaagagaggaatcaagagacgtgtccacatgaagacatttgcgcacacccgtgaatc 1143
QY 591 gccgcgccgggaagctcttctggagggaagagtaagaagccccccacgagacatctgagc 650
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1144 ctggcccccgaggtgtgtggaagaacatgaactac---ggcggtcagtggaactgtgtgggg 1200
QY 651 ctgggctgtgtgtcgtacgtctgtcgtgtctcgtctccctcgtatggtggtcctaactg 710
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1201 ctgggctgtgtgtcgtacgtctgtcgtgtctcgtctccctcgtatggtggtcctaactg 1260
QY 711 ccgaagctgagacagcggtgtgtgtggaagcgccgtctccgacatcccttcttaattctcaa 770
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1261 gagaagcttcttgagctacatcctcatgtgagaagatccgcttcccgacagcttgttccc 1320
QY 771 gactgtgagagcgtgatccgcgcgatgtgtgtgtgagcccc 812
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1321 gaggccaaagctcctgtcttcaagggtgtctcaagaagaagacccc 1362

RESULT 11
US-09-256-465-1
; Sequence 1, Application US/09256465
; Patent No. 6043090
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-2 EXPRESSION
; FILE REFERENCE: RPS-0035
; CURRENT APPLICATION NUMBER: US/09/256, 465
; EARLIER FILING DATE: 1999-02-23
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 1599
; TYPE: DNA
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```

RESULT 12
US-09-289-466-1
? Sequence 1, Application US/09289466A
? Patent No. 6124272
? GENERAL INFORMATION:
? APPLICANT: Brett P. Monia
? APPLICANT: Lex M. Cowsett
? TITLE OF INVENTION: ANTISENSE MODULATION OF PDK-1 EXPRESSION
? FILE REFERENCE: RTS-0060
? CURRENT APPLICATION NUMBER: US/09/289,466A
? CURRENT FILING DATE: 1999-04-09
? NUMBER OF SEQ ID NOS: 86
? SEQ ID NO 1
? LENGTH: 1891
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (81)..(1751)
US-09-289-466-1

```

CLASSIFICATION:

PRIOR APPLICATION DATA:

```
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0465 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1929 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: MMR1D701
CLONE: 472480
US-09-016-000-10
```

```
Query Match          3.8%; Score 96.6; DB 2; Length 1929;
Best Local Similarity 51.3%; Pred. No. 7.1e-12;
Matches 250; Conservative 0; Mismatches 234; Indels 3; Gaps 1;
```

```
OY 60 ggcacagatcagcgccagcagagcccccctcgggtgtttttacagacatcgagcgc 119
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 320 gccacacgctccgcccgcagcctcggagagAACGCCCTGAGACTTCAAGTTGGAAATC 379
OY 120 ctgggcaaggcaactctcggtgtgtgaagctggcgcgatcgagtcaccacacgcag 179
    ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 380 CTGGGGAAGGCTCTTTTTCACGGTGTCTGCGTCGAGAACTGCAACCTCCAGAGAA 439
OY 180 gtggcaataaaatattgataaacac---gattgattcaagcaattggagaatac 236
    ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 440 TAGGCATTAATAATCTGGAGAGCCGATATCATTAATAAGAAAGAGTCCCTATGTA 499
OY 237 tatcgtgaggttcagctgataagctcttgaaacatcacacatcataaagctttacag 296
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 500 ACCAGAGAGGGGATGTCATGCGCGCTGGATCACCCCTTCTTTGTAAGCTTTACTTC 559
OY 297 gttatggaacaaagacatgctttacatcgtcaactgaaattgtcctaaatggagaatg 356
    ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 560 ACATTTGAGGACGACGAGAGCTGTATTTGCGCTTGTATGCAAAATGGAAGACTA 619
OY 357 ttgatatttgacttccacacgggacactgagtggagaagcagcggaagaattctg 416
    ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 620 CTTAATATATTTCGCAAAATCGGTTCTTCATTCGATGAGACCTGTACCGATTTTACAGGCT 679
OY 417 caaatcctgtcgccgtgtgagtaactgtcacgacatcacatcgtccacggagactcaag 476
    ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 680 GAGATTGTCTGCTTGAAGTACTTGACAGGCAAGGCATTCATTCACAGGACCTTAA 739
OY 477 accgagaacctcctgtgtgagtgcaacatgacaatcaagctgtgcagatttgattggg 536
    ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 740 CCGGAAACATTTTGTAAATGAAGATGTCACATCCAGATTTTGGAAACAGCA 799
OY 537 aatttct 543
    ||| |||
DB 800 AAAGTCT 806
```

```
RESULT 14
US-09-289-466-2
; Sequence 2, Application US/09289466A
; Patent No. 6124272
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowert
; TITLE OF INVENTION: ANTISENSE MODULATION OF PDK-1 EXPRESSION
; FILE REFERENCE: RTS-0060
; CURRENT APPLICATION NUMBER: US/09/289,466A
```

```
; CURRENT FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 86
; SEQ ID NO 2
; LENGTH: 1890
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (80)..(1750)
US-09-289-466-2
```

```
Query Match          3.8%; Score 95; DB 3; Length 1890;
Best Local Similarity 51.1%; Pred. No. 1.6e-11;
Matches 249; Conservative 0; Mismatches 235; Indels 3; Gaps 1;
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```
OY 60 ggcacagatcagcgccagcagagcccccctcgggtgtttttacagacatcgagcgc 119
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 281 gccacacgctccgcccgcagcctcggagagAACGCCCTGAGACTTCAAGTTGGAAATC 340
OY 120 ctgggcaaggcaactctcggtgtgtgaagctggcgcgatcgagtcaccacacgcag 179
    ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 341 ctggggaagcctcttttccacggttctgtcgtcgagacatgcaacctccagagaa 400
OY 180 gtgcaataaaatattgataaacac---gattgattcaagcaattggagaatac 236
    ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 401 tatgattaaatcttggagaagcgacatatacataaagaagaacagttccctatgta 460
OY 237 tatgtgaggttcgtgtgataagctcttgaaacatcacacatcataaagctttacag 296
    ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 461 accgagaagcggtgtgtatgtatgtcgtcgtgatacaccctcttgttaagctttactc 520
OY 297 gttatggaacaaagacatgctttacatcgtcaactgaaattgtcctaaatggagaatg 356
    ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 521 acatttcagcgacgaagaaacatgattcgtcgtcttattatgccaanaatggagaacta 580
OY 357 ttgatatttgacttccacacgggacactgagtggagaagcagcggaagaattctcg 416
    ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 581 cttaaatatttcgaaatcggttcatctgattgagacctgttaaccgattttacacggtc 640
OY 417 caaatcctgtcgccgtgtgagtaactgtcacgacatcacatcgtccacggagactcaag 476
    ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 641 gagatgtgtcgtcttgaagtaactgtcacggaagggacatcattcaagagacttaaa 700
OY 477 accgagaacctcctgtgtgagtgcaacatgacatcaagctgtgcagatttgattggg 536
    ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 701 ccggaacacatttgttaaatgaaagataatgcaatccagatccagatttggacaagca 760
OY 537 aatttct 543
    ||| |||
DB 761 aaagtct 767
```

```
RESULT 15
US-09-467-082-3
; Sequence 3, Application US/09467082
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowert
; TITLE OF INVENTION: ANTISENSE MODULATION OF PKA CATALYTIC SUBUNIT C-ALPHA EXPRESSI
; FILE REFERENCE: RTS-0088
; CURRENT APPLICATION NUMBER: US/09/467,082
; CURRENT FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 3
; LENGTH: 2549
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (81)..(1136)
; NAME/KEY: unsure
; LOCATION: 6
```

OTHER INFORMATION: unknown
US-09-467-082-3

Query Match 3.5%; Score 88.4; DB 4; Length 2549;
Best Local Similarity 47.5%; Pred. NO.4.5e-10;
Matches 365; Conservative 0; Mismatches 391; Indels 12; Gaps 3;

```
QY 78 cagaagccctccggttggttcttaacgacatcgagcccttggtgcaagcgaactc 137
Db 186 cagaacacagccacttgatcagttgaacgaatcaagaccctcgacggctccttc 245
QY 138 gcggtgtggaagctgacggtgacatcgatcaccacaacgcaagttgcaataaataatt 197
Db 246 gggcggtgtagctgtgtgaacaacaggaacgggaaccactatgcatgaagatccctc 305
QY 198 gataaacaagattag---attcaagcaatttgagaataatctatcgtgaagttcagctg 254
Db 306 gacaacaagaagtggtgtgaactgaacagatcgaaacacacccctgaatgaanaagcgatc 365
QY 255 atgaagctctgaaccatcacatcaataaagctttacaggttatgtgaanaacaagagac 314
Db 366 ctgcaagctgcaacttcgcttcgttccgttcaaacctcgatctccttcaagacactca 425
QY 315 atgcttaccatcgtaactgaatttgctaaatgtgaagaatgttgattatctgacttcc 374
Db 426 aactatcacatggtcatgtagtaacgtgcccggcggtgagatgttctcacacctacgycgg 485
QY 375 aacgggcaacctgtagtaagaacgagcgcggaagaagttctggaataatcctgtgcgcgtg 434
Db 486 atcggaaggttcagtgagcccatgcccgtttctacgctcgcccaatcgtcctgaactt 545
QY 435 gagtactgtcagacatcacatcgttcacacggagactcaagaaccgagaacctctgtctg 494
Db 546 gagatctgcatcgtctgtagtcatctacacaggaacgagccggaatctgctcatt 605
QY 495 gatggcaacatggacatcaatgaacttgacatttggaatttggaattcttaacagtcagga 554
Db 606 gaccagcaggggtcatcatcaggtgacagacttcggttccgccaagcgctgaag----- 659
QY 555 gaggcctgttccacgtgtgtgtggaagcccccgtatgcccgcgcgggaagctcttgaaggg 614
Db 660 ggcgcgacctgagacctgtgcygcaacccctggtacactgcccctgagatatcctgagc 719
QY 615 aaggaagtatgaagcccccaactgtgacatctggaagcctggtggtgtgtctgaagctcctg 674
Db 720 aaaggtactaacaacaaagcc--gtggaactgtgtggccctgtgggttcttatctatgaatg 776
QY 675 gtctgcgttcttcccttgcgtatggtggtactgcccgaagcgtgaagcagaacggtgtctg 734
Db 777 gccgctgtgtaccgcccttcttctgcagaccagcccatccagatctatgaagaatctgtc 836
QY 735 gaaggcgcttcgcgcatcccttctcatgtctcaagactgtgaagacgtatcgccgcgcg 794
Db 837 tctgggaaggtgtgcttcccttccacttcaagctcgtgaatgaagactctgtcgtggaac 896
QY 795 atgtgtgtgtgtgaaccccgcaagcgcatcaccatcgcccaagatccgg 842
Db 897 ctctctgagtagatctcaccaagcgttctgtggaactcaagaatggg 944
```

Search completed: March 22, 2002, 13:20:03
Job time: 8941 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd

OM nucleic - nucleic search, using sw model

Run on: March 22, 2002, 12:14:54 ; Search time 2393.83 seconds
(without alignments)
11814.911 Million cell updates/sec

Title: US-09-787-559-4

Sequence: 1 cccgcgagcagcagcagcgcg.....aaaaaaaaaaaaaaaaaaaaa 2632

Scoring table: IDENTITY_NUC

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :
EST: *
1: em_estfun: *
2: em_esthum: *
3: em_estlin: *
4: em_estlom: *
5: em_esttpl: *
6: em_esttba: *
7: em_esttro: *
8: em_esttov: *
9: em_hlcc: *
10: gb_estl: *
11: gb_estt2: *
12: gb_hlc: *
13: gb_gss: *
14: em_gss_fun: *
15: em_gss_hum: *
16: em_gss_inv: *
17: em_gss_pln: *
18: em_gss_pro: *
19: em_gss_tod: *
20: em_gss_vit: *
21: em_gss_other: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
1	649.2	24.7	701	11	B6719047	BG119047	602699166
2	493.4	18.7	497	10	AW503500	UI-HF-BND	AW503500
3	344.8	13.1	924	11	BE783804	BE783804	602109724
4	325	12.3	2411	12	AK011789	Mus. musculus	AK011789
5	298.6	11.3	315	10	BE242296	BE247296	TCBAP1E04
6	285	10.8	1076	11	BF537120	BF537120	602049032
7	280.8	10.7	646	11	BF534711	602048240	BF534711
8	273.8	10.4	439	10	A1466101	A1466101	vw40h03.y
9	267.2	10.2	586	10	AV612708	AV612708	AV612708
10	267	10.1	763	11	BE795309	BE795309	601586611
11	265.4	10.1	677	11	BE900808	BE900808	601674532
12	261.6	9.9	435	10	A1528387	A1528387	u196h01.y

[illegible]

ALIGNMENTS

RESULT	1
LOCUS	BG719047
DEFINITION	BC719047 701 bp mRNA EST 08-MAY-2001 602699166F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4831049 5' , mRNA sequence.
ACCESSION	BG719047
VERSION	BG719047.1 GI:13998234
KEYWORDS	EST .
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eumayorita; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 701) NIH-MGC http://mgc.nci.nih.gov/ . National Institutes of Health, Mammalian Gene Collection (MGC)
AUTHORS	Unpublished (1999)
TITLE	Contact: Robert Strausberg, Ph.D.
JOURNAL	
COMMENT	

FEATURES

Source

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/cclone="IMAGE:4831049"
/cclone_1b="NH_MGC_97"
/lab_host="DH10B"

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Db	423	GGGTCGCAGTCGCCACCCCACTGCTGCAGGCTCAGGGGGGCTTGGAAGAGCTTTCT	482
Oy	1811	gcctccctgtcagctt	1825
Db	483	GCTCCCTGTGACGCTT	497
RESULT	3		
LOCUS	BF783804		
DEFINITION	BF783804	924 bp	EST
	602109724F1 NCI_CGAP_Kid14 Mus musculus	CDNA clone IMAGE:4238068	12-JAN-2001
ACCESSION	BF783804	5', mRNA sequence.	
VERSION	BF783804.1	GI:12088840	
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus		
TITLE	1 (bases 1 to 924)		
COMMENT	NIH-MGC http://mgc.nci.nih.gov/ .		
	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		

Tissue Procurement: Jeffrey E. Green, M.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MCC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: L1AM9848 row: p column: 05
 High quality sequence seq: 661.

FEATURES	Location/Qualifiers
source	1. .924

BASE COUNT	ORIGIN
214	a
322	c
246	g
142	t

Query Match	13.1%	Score 34.4.8	DB 11	Length 924
Best Local Similarity	73.4%	Pred. No. 1.3e-38		
Matches 511	Conservative 0	Mismatches 172	Indels 13	Gaps 5
Qy	882	ctgacatccgcgcatgctgtgtgtgagaccgcgcagcgcataccatctgccagatccgg	941	
Db	2	ctgattcaaacgcgcatctgtgtctgtgaccccccctaaagccgcatcaccatataccagatccgc	61	
Qy	942	cagacccggtgtagtgcgggcttgagcccttcgtgcgcggagaccgcctctgcgcgcctttcc	1001	
Db	62	cagcacccggtgatccagcccgacccctctctctgcagcagatgacctctcttgcac	121	
Qy	1002	gcacacagctacacctcgcacaccttggcgactcgaatgagcagcgcttgatcatgcaag	1061	
Db	122	atgcgaagctctaacctctccaaacctggcgcaactcaacagaaacagctctgattatgcag	181	
Qy	1062	acccttgggcgtgagaccgcagagacggttgagagttacttcgaaagaacagcagctataaac	1121	
Db	182	gcccttcggcattgcaccggcagcgagcactatagagttctctgcacaagaacgactacacac	241	
Qy	1122	tttgctgcatttattacctctccctctgagcgctcaagaagatcgcgaatgcccag---	1178	
Db	242	ttttggccgcatattactctctactctcagcgcctctcaagagacatcgaagcccccagccc	301	

Oy	1179	--tgccccgcgcccggcgccctcgcagagccgcgcgcgttcgtgagtctgcgaactcaatg	1233
Db	302	TGATCCGGGGCCACCCCTGAGACCACAGACGCCCGCCAGCTCCGAAGTCTGAGACTTAGAG	361
Oy	1235	ttagaagtgctcactagaagaagtccttccacaccgaccttcgcgaacct-ctgcctgccc	1293
Db	362	TCTGGAGTTTCCTCAGAATAATTCTCCCGTGACCTTTTCCGGCCCTCTCTGTCTGTGCC	421
Oy	1294	cgcagccgcagaaaccttgcctgcaglcgcctccacagccgagatbgactctgtgacctcaga	1355
Db	422	CACAGCCCCAGGCCTTGCTCAGTGTCTCTCCGAGCTGAGTAAGCTGTGATCTTCACA	481
Oy	1354	gctcgcctgcagctgagccctcttcttcccggtgatatgcagctgcgagcgaatgcttcgyc	1413
Db	482	GCTCACTTCA--GCCTTATTATTATCTCCCTCGGATACCAATGCACTGGAGTTCGG-	537
Oy	1414	ccgggccgctgtccccaagagagctcgtctgaca-cagcatcaagttagaaggccagag	1472
Db	538	CACATCCATCTCCCCACGACAGTCTGTGTGACACCGATATCAGCGAGGAGGCCAGCGAG	597
Oy	1473	ggcgccggccttaagagagagagcagagacagcagaagcttccctgccagcagcacgycgg	1533
Db	598	GTCCACAGCTGGAGAGGAACAACAGGAGTGCAGAGAACCCCGTAGACCGGAACAGAGGGG	657
Oy	1533	aggcacacccctgcgcgaagctctccaccgcctctcc	1568
Db	658	AGGCACACAAATAGCTGAAGTCTCCAGCCATTTC	693

RESULT					
4					
LOCUS	AK017789				
DEFINITION	AK017789	2411 bp	mRNA	HNC	05-JUL-2001
ACCESSION	AK017789	Mus musculus	8 days embryo cDNA,	Riken full-length enriched library,	clone:5f30525022, full insert sequence.
VERSION	AK017789				
KEYWORDS	AK017789.1	GI:12857214			
SOURCE	CAP trapper.				
	CAP trapper. (strain:C57BL/6J) 8 days embryo cDNA to mRNA.				

ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL

Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Rodentia: Sciurognathi, Muridae, Murinae: Mus 1 (bases 1 to 2411)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Methods in enzymology. 303, 19-44 (1999)

REFERENCE	AUTHORS	TITLE	JOURNAL	PUBLISHED
2 (bases 1 to 2411)	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komou, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	Genome research. 10 (10), 1617-1630 (2000)	
3 (bases 1 to 2411)	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,			

TITLE	JOURNAL	MEDLINE	PUBMED	REFERENCE
RIKEN Integrated sequence analysis (RISA) system -384-format sequencing pipeline with 384 multicapillary sequencer	Genome research. 10 (11), 1757-1771 (2000)	20530913	11076861	4 (bases 1 to 2411) The RIKEN Genome Exploration Research Group Phase II Team and the


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Db      601  AACGCTGACTCTGGAGCAATCATGAAGACAAATGCAT 641
RESULT 7
BF534711 646 bp mRNA EST 11-DEC-2000
LOCUS 602048240F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4187769 5',
DEFINITION mRNA sequence.
ACCESSION BF534711
VERSION BF534711.1 GI:11622074
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 646)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaaps-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L1AM9510 row: p column: 10
High quality sequence stop: 646.
FEATURES
Source
Location/Qualifiers
1..646
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_image="4187769"
/lab_host="NCI_CGAP_SG2"
/Note="Organ: salivary gland; Vector: PCWV-SPORT6; Site:1;
NotI; Site:2; SalI; Cloned unidirectionally. Primer: Oligo
dT. Average insert size 1.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 172 a 153 c 178 g 143 t
ORIGIN
Query Match 10.7%; Score 280.8; DB 11; Length 646;
Best Local Similarity 67.6%; Pred. No. 9.7e-30;
Matches 438; Conservative 0; Mismatches 207; Indels 3; Gaps 3;
Oy 172 gccacagaaagtcctcgggtgttttaacacacagcggagccggcgaagca 231
Db 1 GGGGTCATAGCCGCCGTCGCATCGGCTACTACGAGATGCACCGCACATCGGAGGGA 60
Oy 232 acttcggtgtgtgaagctggtcgcgcatcgagtcacacaaacgcaagttgcaataaa 291
Db 61 ACTTGCTGTGTGTCAGAGCGGGCCAGCACCTGCTGACCAAGGCAAGTTGCTATTAAAA 120
Oy 292 taattgataaaacagattagattaaagcaatttgagaa-aattatcgtgaagttcg 350
Db 121 TCATGATTAAGAGCCAGCTGATGAAGAAACCTTGAAGAGATTGTTCGGAGAGGTTCAG 180
Oy 351 ctgataagagctctgaacatcacacatcataaagcttaccaggttaaggaaacaag 410
Db 181 AATAATGAAGATGCT-TGCCATTCACACATCATCATCACTTACCAAGTCTATGAGACAGAG 239
Oy 411 gacatgcttacatcgtcactgaattgtctaaaaatggagaagtgttgatattatgact 470
Db 240 CGCATGATTTACTGCTGACAGATATAGCTAGCGGAGGAGATATTGACCACTTGCTGA 299
Oy 471 tccacgggacactgagtggagaagcgcggaaggttcctgcaaatcctgtcgcc 530

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Db      300  GCCCATGGAAGATGCGACAGAAGAGCTCGACGGAAGTCAACAGATCGTACACGCG 359
Oy 531 gtggagtagtgcacgacatcaatcgcacccggagacctaaagcggaaacctccg 590
Db 360 GTGATTTTGTGCTACTGTGGAATATGCTTCATCTGATTTAAACCGAANAATTACTT 419
Oy 591 ctgataagacaatgacatacaagctgcagatttgagatttggaattctacaagta 650
Db 420 CTGGAGCGCAATCTGATATCAAAATAGACAGACTTTGGCTTCAGCAACTCTTCACTCA 479
Oy 651 ggaagacctctgtccacgtgtgtgtggagaccccgatgcgcgcccggaaagtcctgag 710
Db 480 GC-CAGATGCTTAAGACGCTGTGTGCGACCCCTCCCTATGACCGCCCAAGAGCTTTTCGAA 538
Oy 711 ggaagagtagtgaagagcccgacgctgcagatctgagcctggcgtgtgtcgtcgc 770
Db 539 GGGAGGAATATGATGCGCCCAAGTGCACATATGAGGCTTGGATTGTCTCTATGTG 598
Oy 771 ctgctcgtgtctctcctccttcgattggcctaactgcgcagcgtg 818
Db 599 CTGCTGTGTGCGGCCCTGCCGTTTGTATGGAGACACTCGACATCTG 646
RESULT 8
A1466101 439 bp mRNA EST 09-MAR-1999
LOCUS A1466101
DEFINITION v440h03.y1 Soares mammary gland NBMG Mus musculus cDNA clone
IMAGE:1246325 5' similar to SW:MSK MOUSE 060670 PUTATIVE
SERINE/THREONINE-PROTEIN KINASE MSK ;, mRNA sequence.
ACCESSION A1466101
VERSION A1466101.1 GI:4320131
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 439)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaaps-remail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:660013
This read is a RESEQUENCE of a previously sequenced mouse clone
This read has been verified (found to hit its original self in the
correct orientation)
Seq primer: -40RP from Glibco
High quality sequence stop: 380.
FEATURES
Source
Location/Qualifiers
1..439
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_image="1246325"
/lab_host="NCI_CGAP_SG2"
/Note="Organ: mammary gland; Vector: pT73D-Pac (Pharmacia
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
primer 15.
TGTTCACCAATCTGAAGTGGAGCGCGCCGCAAGTGTGTTTTTTTTTTTTTTTTTTTTT
T 3'J); double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo."

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ORIGIN	BASE COUNT	87 a	157 c	107 g	88 t
Query Match	10.4%;	Score 273.8;	DB 10;	Length 439;	
Best Local Similarity	78.3%;	Pred. No. 1e-28;			
Matches 342;	Conservative	0;	Mismatches 92;	Indels 3;	Gaps 1;
Oy 1209	cgagcttgagctcgagacctcagtggtttgttgaggtgtgctcagaagagttcttcacccgac	1268			
Db 5	CAGCTCCCAAGCTCAGACCTCAGAGTCTGGAGGTTCTCAAGAAATTCTCCCGTGTAC	64			
Oy 1269	cttttcgaccctgctgtgtgcccggagccgagacctgtgtgacgcgtctccag	1328			
Db 65	CTTTTCGGGCCCCCTCTCTGCTGTGTCACACAGCCCCAGGCGCTTGGCTCAGTCTGTCTGCAG	124			
Oy 1329	gccgagatcgagctgtgagctccaagagctcgtctgacgtgtgacctgtgtctccaggtgat	1388			
Db 125	GCTGAGATAGACTGTGATCTCCACAGCTCACATCTCA---GCCCTTATTATTCCTCCCTGAT	181			
Oy 1389	gccagctgcagcgagagtggttccggcccggcccgtgtctcccaagcagcctgtgtgacaca	1448			
Db 182	ACCAACTCAGAGTGAGTGTTCGGGACCGAGTCCATCTCCCAAGCAGTCTGTGTGACACA	241			
Oy 1449	gccatcagtgaggagccagcgaggggcccgggacctcagaaggagagagcagagacgcagga	1508			
Db 242	GCTATTCACCTGAGGAGGCGCAGGCGAGGTCACACCTATAGGAGAACAGAGTCTCAGGA	301			
Oy 1509	tcacctgcagcagcagcagggcgccgagagacacacctgtgagcttcacaccgctctcc	1568			
Db 302	CCCCGCCCCGGAAGCACAGGCCGGAGGACACACATTGGCTGAAGTCTCCACCCATTCTCC	361			
Oy 1569	ccactcacgcgcacatgatatgtctgtctccctccacacagcgcaagtcctgtcagaaggga	1628			
Db 362	CCGCTCAACCTCTCTGTGATTAATTGTCTCTCTCTGCGACGCGAGTCCCGGAAGGG	421			
Oy 1629	accagctctgacagttg 1645				
Db 422	ACCAGCTCCGACAGCTG 438				
RESULT 9	AV612708				
LOCUS	AV612708	586 bp	mRNA	EST	30-AUG-2000
DEFINITION	AV612708 Bos taurus lung fetus Bos taurus cDNA clone E11U047B05 5',				
ACCESSION	AV612708				
VERSION	AV612708.1	GI:9748378			
KEYWORDS	EST.				
SOURCE	COW.				
ORGANISM	Bos taurus				
REFERENCE	Ennajirola; Metazoa; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mumallia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;				
	Bovidae; Bovinae; Bos.				
	1 (bases 1 to 586)				
	Sugimoto,Y., Hirotsune,S., Takasuga,A., Itoh,R., Jitohzono,A. and				
	Suzuki,H.				
TITLE	bovine cDNA sequencing				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Yoshikazu Sugimoto				
	Animal Genetics Division				
	Shirakawa Institute of Animal Genetics				
	Odaikura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan				
	Tel: 81-248-25-5641				
	Fax: 81-248-25-5725				
	Email: kazusugie@ocn.ocn.ne.jp				
	Single pass sequencing.				
	This clone was obtained from a polyA-deleted cDNA library.				
FEATURES	Location/Qualifiers				
SOURCE	1..586				
	/organism="Bos taurus"				
	/db_xref="taxon:9913"				
	/clone="E11U047B05"				

BASE COUNT		135 a	143 c	165 g	143 t	
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	/clone_lib="bos_taurus_lung_fetus"					
	/tissue_type="lung"					
	/dev_stage="fetus"					
	/lab_host="DH10B"					
	/note="Vector: pZL1; Site_1: SalI; Site_2: NotI; Poly A was deleted from a NotI site"					
Query Match	10.2%; Score 267.2; DB 10; Length 586;					
Best Local Similarity	67.8%; Pred. No. 7.5e-28;					
Matches	388; Conservative 0; Mismatches 103; Indels 1; Gaps 1;					
OY	386 gcttacccaggctatgagaaacgaagacatcgtttacatcgctactgaatttgctaataa	445				
Db	12 gctttaccaggtcatgatgagacagacggatgatatttatctgtagacagaatatgctatgg	71				
OY	446 ttgagaatgttgtatttatttgactccaacgggcaccttgatgagaacggcgcgaa	505				
Db	72 AGGGGAATATTTTGACCCCTGTGTGCCACCGCAGCATGCAGAAAGAGAGCCCCGTCG	131				
OY	506 gaadtttcgcaaatccctcgtcgcgcgttgagtactgttaacgccatcacatcgtccacg	565				
Db	132 CAAGTTCACAACAGATCGTTGACGCCGCTGATTTTTTGCTACTGTGCGAATGTTTCATCG	191				
OY	566 gaacctcaagacgcgagaacctcctgtctgtgaatgagacaatgacalcaaacctgcacatt	625				
Db	192 TGATTTTAACCTGAAAATTTGCTCCTGACGCCCAATCTGAATATCAAGATTAGCAGATT	251				
OY	626 ttgatttgggaattctctacaagtcagaagagcctctgtccacgttggttggagagcccc	685				
Db	252 TGGCTTCAGTAACCTCTTACCCTCGGGCACCTACTGAAGACCTGTGTGCGACGCCCTCC	311				
OY	686 gtatgcccgcgcgcgaagcttcttggagggaagagatgaagggccgcgcggagacatgt	745				
Db	312 CTATGCTCTCTCTGAACCTTTTGAAGGAAGAAGATATACGAGACCCAAGTGGACATCTG	371				
OY	746 gagctgtggcgttgctgtctgtactgtctgtcgtgctctctcccttcgattggcccaa	805				
Db	372 GAGCTCGGAGTCTGTCCTCTATGTGCTTGTGTGGGGGCCCTCGCGTTTGAATGGAGACAC	431				
OY	806 ccgtgcgaagcttgagacaagcggtgtctgtgaggggccgcttcgcgatalccctcttcat	865				
Db	432 ACTGCAGAACTGTGCGGGGCCGGGTGTGAGTGGAAAGTTTGCAATCCATTTTATGTGC	491				
OY	866 tcaagactgttgaagagcctgtatccgcgcgcgacatgtctgttg-tgaacccgcgcagcgac	924				
Db	492 CACGGAATGTAGGACCTGTGATCCGCCCTATGCTGTGGTGTGGACCCCAAGCGCCCTCT	551				
OY	925 ccatacgcacacatccgcgcgacgcggttgatg	956				
Db	552 TCATGGAGACATCTGCAAGCCCAAGTGGATG	583				

RESULT 10

LOCUS	BE795309	763 bp	mRNA	EST	20-SEP-2000
DEFINITION	60158661fl1 NIH_MGC_7 Homo sapiens CDNA clone IMAGE:3940970 5' ,				
ACCESSION	BE795309				
VERSION	BE795309.1 GI:10216507				
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabs@remail.nih.gov				

Db 121 AAGTAAAAAAGCTCTACCTATATCATGAAATATCAAGTGAAGTATTGACT 180
Oy 463 attgacttccacagcgccactgagtagaagcggcggaaagttctggcaatcc 522
Db 181 ATTGGTTGCACATGACGAGATGACGAAAAAGAACCAAGATCTAAATTAGACAGATTG 240
Oy 523 tctggcgctgagtagctgtcaacgacatcaatcgtcagcgagaccctcaagacggaga 562
Db 241 TGTCTGCACTTCAATATCTCCATCAGAAACGGATCTACATCGACACTCAAGCTGAAA 300
Oy 583 accctctgtctgtagtgaacatgacatgaagctgacagatttgattgggaattctc 642
Db 301 ATCTATTGTTAGTGGCGATATGAAATACATTAATACAGATTTCGGTTTACCAATGAAT 360
Oy 643 acaagtcagagagagcctctgtccacgttggtgagagccccccgtatgcccgcccggaag 702
Db 361 TTACTGTTGGCGGTAAACTCGACACGTTTCGTGGCAGTCTCCATACGACGACCTGAGC 420
Oy 703 tcttgaaggggaagagtagtgaagcccccaagctgagacatctggaagcctggcggtgtgc 762
Db 421 TCTTCCAGGGCAAGAAATATGACGGCGCAGAAAGTGTGATGTGAGTCTGGCGTCTATT 480
Oy 763 tctagctctgtctgctgctctctccctctgtagtgagcctaacctgcgacgctgagac 822
Db 481 TATACACTAGTACGCTGCTCCTCCTCGATGGCAAAACCTTAAGAACTGAGAG 540
Oy 823 agcgggtgtctgagggcgccctccgacatccctctctcatgtctcaagactgtgagagcc 882
Db 541 AGGAGTATACGAGGCGCAATACCGAATTCCCTTACATGCTACAGATGTGGAAGAAC 600
Oy 883 tgaatccgcatgtgtgtgtgtgagaccccgagcgcatcacatcgccagatccggc 942
Db 601 TTCTCAACGTTTCCGTGCTTAATCAATTAACGGCGGCTCTGAGCAATCATGA 660
Oy 943 agcaccggtgagatgc 957
Db 661 AGGACAGGTGATCC 675

RESULT 12
LOCUS A1528387 435 bp mRNA EST 18-MAR-1999
DEFINITION U196h01.y1 Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1890289 5', mRNA sequence.
ACCESSION A1528387
VERSION A1528387.1 GI:4442522
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 435)
AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,
B., Smaller,T., Gibbons,M., Pepe,D., Harvey,N., Schur,R., Ritter,
E., Kohn,S., Shin,T., Jackson,M., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
CONTACT: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LML: contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:974613
Seq primer: custom primer used
High quality sequence stop: 429.

FEATURES
source 1.435
/organism="Mus musculus"

/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:1890289"
/clone_lib="Sugano mouse liver mlia"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: Liver; Vector: pME18S-FL3; Site_1: DraIII
(CACTGTG); Site_2: DraIII (CACCATGG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTCGCGCTTTTCTTTTCTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTGGCGTACGCG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTG, 3' site CACCATGG). XhoI should
be used to isolate the cDNA insert. Site selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTCTGCTGTAAAGCTGG and 3' end
primer CGACGTGACGTCGACCA."

BASE COUNT 80 a 150 c 125 g 80 t
ORIGIN

Query Match 9.9%; Score 261.6; DB 10; Length 435;
Best Local Similarity 76.6%; Pred: No. 4.9e-27;
Matches 334; Conservative 0; Mismatches 99; Indels 3; Gaps 1;

Oy 1591 tctctccctccacagcggaactctctgagagggaacagctgacagtgtctga 1650
Db 2 TTGCTCTCTCTCTGCGACGCGAGTCCCTCGAAGGAGCAGCTCCGACGCTCTCC 61
Oy 1651 cctctctcgagaaagcccgcggggtcagltgacaccccgccactcaagggtctgc 1710
Db 62 CTTCTCTGCAAGTGAAGGTCCTGACAGGCTTGACAGGCGCTGCGCACCCAGGCGTC 121
Oy 1711 tggggcctctcccggtcaggtcgtcgtccctctcgagggtcgagtcgcaccc 1770
Db 122 TGGGACACGAGCTTCAGATGAGATTGGCTCGCCCTTCTGAGATCAGACACGCC 181
Oy 1771 cagtgctcagagctcaggggggttgaggagagctgtctcctcccgctcagctccag 1830
Db 182 CTGTGCTCCAGACTCAGGACAGGTGTGGGACACGCGCTTACCTCCGTCAGCTTCCAG 241
Oy 1831 agggacggcgggcgtcgagacactcactgactcaagagctgaaagcctctcgagcagc 1890
Db 242 AGGGACGGAGGCGTCTGATATCTCTCACTCAAGGGGCTGAAGGCTTCGGGACGAGC 301
Oy 1891 tgaagaaagcagcgagaccaaagggttctggaactgaaacaaatcaagggtcgtc 1950
Db 302 TGAGGAAAAATGCGAGGACCAAGGGGTTCTCGGAGACTGAAACAGATCAAGGTTGGCTC 361
Oy 1951 gccaggtgtccagagctcccgccagcgcgggcgagcagggcggtcagccctcagc 2010
Db 362 GCCAGGTGTGCGCA--TCTCTCCGTCGGAACCTCCCGGGGAGGATGATCTTCCACA 418
Oy 2011 cccctgacagagccc 2026
Db 419 CCCGAGCCCCAAGCTC 434

RESULT 13
LOCUS AUI32239 866 bp mRNA EST 24-OCT-2000
DEFINITION AUI32239 NT2RFP3 Homo sapiens cDNA clone NT2R304052 5', mRNA
sequence.
ACCESSION AUI32239
VERSION AUI32239.1 GI:10992593
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE	1 (bases 1 to 866)
AUTHORS	Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.
TITLE	HRI human cDNA project
JOURNAL	Unpublished (2000)
COMMENT	Contact: Takao Isogai Genomics Laboratory Helix Research Institute 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan Tel: 81-438-52-3951 Fax: 81-438-52-3952 Email: genomics@hri.co.jp HRI human cDNA project: 5'- & 3'-end one pass sequencing: Helix Research Institute: cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.
FEATURES	Location/Qualifiers
source	1..866 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="NT2RP304052" /clone_lib="NT2RP3" /cell_type="teratocarcinoma" /cell_line="NT2" /note="Vector: PME18SFL3; mRNA from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA) induction"
BASE COUNT	304 a 150 c 191 g 217 t 4 others
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Best Local Similarity	61.5%; Pred. No. 4.9e-27;
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QY	347 tcaagctgtgaagcttcggaaccacacacatcaataagcttcacagattatgaagac 406
Db	61 AAGATTAATGAAGATTTTAAATCAATCCCAATTAATGAAATTATTCGAAGCATTTGAAC 120
QY	407 aaagacatgcttcacatcgttcactgaatttgcctaaaaaayggagaatgcttgattat 466
Db	121 TCGAAAAACACTCTACCTAATCATGTGAATATGCAAGTGGAGGTGAAGATTGTGACTATT 180
QY	467 gaactccaacgggcaaccctggagtggagaagggcgggagaagatcttcgcaatcctgtc 526
Db	181 GGTTCACATATGGCAGATGAAAGAAAAAGAACAAAGATCTAATTTAAGACAGATTGTCTC 240
QY	527 ggcctgtgaagtactgtcaagcacatcaaatcgttcacccgggagacctcaagaccggaacct 586
Db	241 TGCAGTTCATATCTCCATCGACAAAGACGATGTACATCGAGACCTCAAGGCGTGAATACT 300
QY	587 cctgcttgatcgtgaacatcgtgaacataagctctgcagatttggatttggaaattctacaa 646
Db	301 ATTGTTAGATGCGATATGAAACATTAAAAATGACAAATTTCGGTTTTACCAATGAAATTAC 360
QY	647 gtccaagagacctcgtccacagctgggtgggagcccccgctatccggcccggaagctt 706
Db	361 TGTTCGGCGTAACTCGACACAGCTTTTGTGGCAGTCTCTCAATACGACGACTGTAGCTTT 420
QY	707 tgaagggaaggaagtgaagagccccccagctcgtgaacatctggaagcctgcggctcgtgtcgt 766
Db	421 CCAGGCGAAGAAATATGACGGGGCCAGAAAGTGGATGTGTGGAGTGTGGGGGTCAATTTATA 480
QY	767 cgtccctgtctgcagctcttcgcccttcgtatggagccctaacctgcgcagctcgtgaacggc 826
Db	481 CACACTATTCAGTGGCTACTTCCCTTTGATGGGCAAAACTTAAGCAACTGAGAGAGAG 540
QY	827 ggtgcgtgaagggcgcttcgcacatcccttctcatcgtcctaagactctggaagcgtgat 886

Db	541	AGTATTAGAGGGAANTACAGATTCCCTTCTACATGTCCTACAGACTGTGAAACCTTCT	600
Qy	887	ccgcgcgaatcgtcgtgtgtggaaccccgccagagcgtacacacatcgcccgatccgcagca	946
Db	601	CAACGTTCTCGTGTGCTAAATTCATTAACGCGGACTCTAGACGAATCATGTAAGA	660
Qy	947	ccgtgtgattgcgcgtgtgagc	966
Db	661	CAGGTGGATCAATGCAAGGCG	680
RESULT	14		
LOCUS	BG825423		
DEFINITION	60274683572 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:489824 5',	EST	22-MAY-2001
ACCESSION	BG825423		
VERSION	BG825423.1		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	NIH-MGC http://mhc.nci.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgabbs-remail.nih.gov		
	Tissue Procurement: ATCC		
	cDNA Library Preparation: Ling Hong/Rubin Laboratory		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LMNL at:		
	http://image.lnl.gov		
	Plate: L1CM1792 row: e column: 09		
	High quality sequence stop: 746.		
FEATURES	Location/Qualifiers		
source	1..748		
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	/db_xref="taxon:9606"		
	/clone_image="489824"		
	/clone_id="NIH_MGC_17"		
	/tissue_type="rhabdomyosarcoma"		
	/lab_host="DH10B (phage-resistant)"		
	/note="Organ: muscle; Vector: pOMB7; Site.1: EcoRI;		
	Site.2: XhoI; cDNA made by oligo-dT printing.		
	Directionally cloned into EcoRI/XhoI sites using the		
	following 5' adaptor: GGCACGAG(5). Size-selected >500bp		
	for average insert size 1.8kb. Library constructed by		
	Ling Hong in the laboratory of Gerald M. Rubin (University		
	of California, Berkeley) using zap-cDNA synthesis kit		
	(Stratagene) and Superscript II RT (Life Technologies)."		
BASE COUNT	222 a 163 c 182 g 181 t		
ORIGIN			
Query Match	9.8%; Score 257.4; DB 11; Length 748;		
Best Local Similarity	61.3%; Pred. No. 1.5e-26;		
Matches 448; Conservative 0; Mismatches 281; Indels 2; Gaps 2;			
Qy	215	gaccctgggcaaaaggcaacttcgcggtgtgtggaatcgtgcgcgcatcgatccaccaaac	274
Db	14	GACCATTGTGGCAAGGCTATTTTGGCCAAAGTGTAAGTTGGCCCGACACATCCGACTGGAA	73
Qy	275	gcaggttcaataaaataatctgtataaaacgcgttatgatccaagcaatttggsgaaat	334
Db	74	AGAGGTAGCTGTGAAGATCATTTGAACAGCTCAACTGAACTCTCCAGCCTCCAGAACT	133
Qy	335	ctatgtgaagttcgcgtcgtatgaagctctctgaaacatcaacaatcaataaagcttaca	394
Db	134	ATTCCGCAAGTAAGCAATTAATGAGGTTTGAATCATCCCAACATAGTTAATTAATTGA	193

Search completed: March 22, 2002, 12:15:06
Job time: 5304 sec

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Db 1681 tcagtgacacccggccaccacagggctgtgtggcctgtctcccggtcaagctgacct 1740
Oy 1741 cgcctctcttggtgctcagctcccgccacccacagtgctgcagggctcaggggcttggag 1800
Db 1741 cgcctctcttggtgctcagctcccgccacccacagtgctgcagggctcaggggcttggag 1800
Oy 1801 gaactgtctcgtctcctgtcagcttccaggaaggagcgaggctcgacactactga 1860
Db 1801 gaactgtctcgtctcctgtcagcttccaggaaggagcgaggctcgacactactga 1860
Oy 1861 ctcaaggagcgaaggccttccgagcagctgaggaagacacgcgagcccaaaaggtttc 1920
Db 1861 ctcaaggagcgaaggccttccgagcagctgaggaagacacgcgagcccaaaaggtttc 1920
Oy 1921 tgggactgaacaaatcaaaagggtctgctcagaggtgtccaggttccctgcagcgagg 1980
Db 1921 tgggactgaacaaatcaaaagggtctgctcagaggtgtccaggttccctgcagcgagg 1980
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Db 2101 tgcctcaggtatcacagcaccacccgagcctgcacccgagctgtcccaagcccccagcg 2160
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Db 2521 ctccagagggagtgagacacacacacacacacacacacacacacacacacacacacacac 2580
Oy 2581 caatacgtttaggtgttttggcgaataaataaataaataaataaataaataaataaataa 2632
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```

RESULT 2

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AAx82951
ID AAx82951 standard; cDNA: 2533 BP.
AC AAx82951:
XX 07-JUL-2000 (first entry)
XX Human keratinocyte derived pKer122 encoding cDNA #1.
DE
XX

```

```

KW Keratinocyte; regulatory protein; human; pKer122; antiproliferative;
KW kinase; signal transduction; desmosome; dermatological condition;
KW pemphigus vulgaris; psoriasis vulgaris; epidermis; cosmetic; ss.
OS Homo sapiens.
PN WO200017232-A2.
PD 30-MAR-2000.
PF 06-SEP-1999; 99MO-DE02665.
PR 19-SEP-1998; 98DE-1042863.
XX
XX (KRAM/) KRAMER M.
PI Kramer M, Bechtel M, Reinartz J, Schaefer B, Wallich R;
XX WPI; 2000-283542/24.
DR P-PSDB; AAW90878.
XX
PT New regulatory polypeptide from keratinocytes, useful for diagnosis and
PS treatment of dermatological disorders, also in cosmetics
PS Claim 2; Page 49; 55pp; German.
XX
XX This invention describes a novel human regulatory polypeptide designated
CC pKer122 (I), or its variants from human keratinocytes, which in activated
CC keratinocytes is the same as, or similar to, the most highly expressed
CC protein and has antiproliferative activity. (I) is a kinase involved in
CC signal transduction and is conjectured to be involved in cell-cell or
CC cell-matrix interactions and/or formation of (hemi)desmosomes. Modulation
CC of (I) will affect proliferation and differentiation of keratinocytes.
CC (I) is upregulated in some dermatological conditions, e.g. pemphigus
CC vulgaris and psoriasis vulgaris. (I) is used to raise specific antibodies
CC (Ab) which are used for diagnosis and treatment of dermatological
CC disorders and for cosmetic treatment of the epidermis. Nucleic acid (II)
CC that encodes (I) is used; (II) to produce transgenic mammals (particularly
CC mice and rats); and (II) as source of sense and antisense
CC oligonucleotides for diagnosis and treatment of dermatological disorders
CC and for cosmetic treatment of the epidermis. (II), (I) and polypeptides
CC (Ia) produced by splice variants of (II) are used to identify specific
CC binding agents (potentially useful in medicine and cosmetics) that
CC modulate their function and/or expression, especially inhibitors and
CC activators. Cells and animals transformed with (II) are used to study
CC (I)-induced changes in cell morphology and basic functions. This
CC sequence encodes the human keratinocyte protein pKer122 described in the
CC method of the invention.
XX
XX Sequence 2533 BP; 501 A; 820 C; 762 G; 450 T; 0 other;
SQ

```

Query Match 95.98; Score 2522.8; DB 21; Length 2533;

Best Local Similarity 99.98; Pred. No. 0;

Matches 2524; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 8 aggtgcgcgcgagcagatggtatcatgtcgaagttcagcgcgagcccgcgagcagag 67
Oy 167 tcaaggccagcagaagatccctcgcggttgggttttaacgacatcagcagcctgggcaa 226
Db 68 tcaaggccagcagaagatccctcgcggttgggttttaacgacatcagcagcctgggcaa 127
Oy 227 aggaacttcgagtggttgaagctggcgagcagctgcagtcacaaacgcaggttgaat 286
Db 128 aggaacttcgagtggttgaagctggcgagcagctgcagtcacaaacgcaggttgaat 187
Oy 287 aaaaataatgataaaacacagatcagatcacaagcaatttggagaatactcagtgaggt 346
Db 188 aaaaataatgataaaacacagatcagatcacaagcaatttggagaatactcagtgaggt 247
Oy 347 tcaagtgatgaagcttctgaacacatccacacatcataaagcttaccaggttataagaaac 406

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248 lcaagcttgaaggtcttcgaaacacacacataaaagcttaccgggttaagaaac 307
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Db aagagacatgtcttaacatgcataatgtctaaataatgagaaatgttattt 367
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OY ctgt 1366
Db ctgt 1267
OY ggcctctctctcgcgttgagatccagctgacagcgagtgcttccggcccgcgctgtc 1426
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1328 cccaagagcctgtctggaacagcactcagtgagagagcgaagcgcgagcctaaga 1387
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Db ggaagagagagagacagcagagagctcctcgcccaacagcagcgagcgagcactgtgc 1447
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Db aagcag 1627
OY ggtcag 1786
Db ggtcag 1687
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OY ggaac 1906
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OY ggaac 1966
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2627 aaaaaa 2632
2528 aaaaaa 2533

RESULT 3
AAS06718
ID AAS06718 standard; cDNA; 2361 BP.
AC AAS06718;
XX
XX 12-SEP-2001 (first entry)
XX
XX Polynucleotide sequence encoding human protein kinase #18.
XX
XX Human; protein kinase; PTK; STK; cancer; cardiovascular disease;
KM metabolic disorder; immune related disease; neurological disorder;
KM neurodegenerative disorder; inflammatory disorder; infectious disease;
KM reproductive disorder; gene therapy; ss.
XX
XX Homo sapiens.
OS
XX MO200138503-A2.
PN
XX 31-MAY-2001.
PD
XX 22-NOV-2000; 2000MO-US32085.
PF
XX 24-NOV-1999; 99US-0167482.
PR
XX (SUGC-) SUGEN INC.
PA
XX P10man GD, Whyte D, Manning G, Sudarsanam S, Martinez R;
PI Flanagan P, Clary D;
XX
XX WPI; 2001-343950/36.
DR P-PSDB; AAU03518.
XX
XX Nucleic acids encoding human kinase polypeptides, useful for preventing
PT diagnosing and/or treating e.g. cancer, immune, cardiovascular and
PT neuronal-associated diseases, and microbial infections -
XX
XX Example 1; Figure 1; 433pp; English.
PS
XX AAS06701-AAS06757 encode for novel human protein kinases #1-57. The
CC novel protein kinases have been identified as members of the tyrosine
CC or serine/threonine kinase (PTK and STK) families. The polynucleotides
CC encoding protein kinases and the polypeptides may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate kinase expression. For example, they may be used to treat
CC cancers (especially cancers of hematopoietic origin), cardiovascular
CC disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),
CC immune related diseases (e.g. rheumatoid arthritis), neurological
CC disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.
CC Parkinson's disease), inflammatory disorders (e.g. asthma), infectious
CC disease (e.g. HIV) and reproductive disorders (e.g. infertility).
CC Additionally, polynucleotides encoding protein kinases may be
CC used for gene therapy and as DNA probes in diagnostic assays.
CC The protein kinase polypeptides may be used as antigens in the production
CC of antibodies against the protein kinases and in assays to identify
CC modulators of protein kinase expression and activity.
CC
XX
XX Sequence 2361 BP; 431 A; 784 C; 726 G; 420 T; 0 other;

Query Match 88.4%; Score 2326.6; DB 22; Length 2361;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2348; Conservative 0; Mismatches 4; Indels 9; Gaps 1;

QY 123 atggtatcatatcgtcgaatctcagcgcgagcccgcgagccagatcagggccagcagaag 182
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Db 1 atggtatcatatcgtcgaatctcagcgcgagcccgcgagccagatcagggccagcagaag 60
183 tcctcccggttggttttttacgacatcgaacgagccctgggcaaaaggaacttcgggtg 242
|||||
Db 61 cccctccgggtgggttttttacgacatcgaacgagccctgggcaaaaggaacttcgggtg 120
QY 243 gtagaagctggcgcgatcgagtcacccaacggaaggttcgaataaataatgatataa 302
|||||
Db 121 gtagaagctggcgcgatcgagtcacccaacggaaggttcgaataaataatgatataa 180
QY 303 aacagattagatcgaagcaatttgagaanaatcattctgtaggttcagctatgaagctt 362
|||||
Db 181 aacagattagatcgaagcaatttgagaanaatcattctgtaggttcagctatgaagctt 240
QY 363 ctgaacatccacacatcataaagcttaccaggttatggaacaaagacatgctttac 422
|||||
Db 241 ctgaacatccacacatcataaagcttaccaggttatggaacaaagacatgctttac 300
QY 423 atcgtaactgaatttgctaaataatggagaataatgtttgattttgacttcaacgggac 482
|||||
Db 301 atcgtaactgaatttgctaaataatggagaataatgtttgattttgacttcaacgggac 360
QY 483 ctgagtgagaacgagcgcggaagaagttctggaataatctgtcggccgttgagtaactgt 542
|||||
Db 361 ctgagtgagaacgagcgcggaagaagttctggaataatctgtcggccgttgagtaactgt 420
QY 543 caggaacatcaatcgttccacccggagacctcaagaacggaacctctgtctgtagtgaac 602
|||||
Db 421 caggaacatcaatcgttccacccggagacctcaagaacggaacctctgtctgtagtgaac 480
QY 603 atggacatcaagctggca-----gatttgatttgggaatttctacaagtcagga 653
|||||
Db 481 atggacatcaagctggcaagcagcaggaatttggatttgggaatttctacaagtcagga 540
QY 654 gaggctctgtccacgttggttgtagagcccccgtatgcccgcgggaagcttcttagagg 713
|||||
Db 541 gaggctctgtccacgttggttgtagagcccccgtatgcccgcgggaagcttcttagagg 600
QY 714 aagaagatagaagcccccaacgtgacatctgtaggctgggctgggtggtctgtaagctctg 773
|||||
Db 601 aagaagatagaagcccccaacgtgacatctgtaggctgggctgggtggtctgtaagctctg 660
QY 774 gtcgcggttctcccttcgatacgtgagcctaactgcccgaacgctggaacaacgggtctg 833
|||||
Db 661 gtcgcggttctcccttcgatacgtgagcctaactgcccgaacgctggaacaacgggtctg 720
QY 834 gaggcgcttcgcgacatcccttctcatgtctcaagaactgtgagacgtgataccgcgc 893
|||||
Db 721 gaggcgcttcgcgacatcccttctcatgtctcaagaactgtgagacgtgataccgcgc 780
QY 894 atgctggtgtgtagcccgccgagcgacatcagatcgccagatccggcagcagctgtg 953
|||||
Db 781 atgctggtgtgtagcccgccgagcgacatcagatcgccagatccggcagcagctgtg 840
QY 954 atgaggctgagccctgtcttcgggagcccgccgcccgccttctccgacacagctac 1013
|||||
Db 841 atgaggctgagccctgtcttcgggagcccgccgcccgccttctccgacacagctac 900
QY 1014 acctccaacctggcgacatacagatgagcagcgctgtggtatcatgtagaaccttcggcgct 1073
|||||
Db 901 acctccaacctggcgacatacagatgagcagcgctgtggtatcatgtagaaccttcggcgct 960
QY 1074 gaccggaaggaagcggtggtgtagctacgtcaaaacgagcgtataacacacttgcgcatc 1133
|||||
Db 961 gaccggaaggaagcggtggtgtagctacgtcaaaacgagcgtataacacacttgcgcatc 1020
QY 1134 tattacctctcttgagcgagctcaagagatagatgagatgcccagtcgcccgcggcg 1193
|||||
Db 1021 tattacctctcttgagcgagctcaagagatagatgagatgcccagtcgcccgcggcg 1080

[illegible]

RA	(SUGGE-)	SUGEN INC.	
XX	PI	Plozman GD, Martinez R, Whyte D, Sudersanam S;	
XX	DR	WPI: 2001-032161/04.	
XX	DR	P-PSDB: AAB65631.	
XX	XX	Nucleic acids encoding kinase polypeptides, useful for diagnosing and treating immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers -	
XX	XX	Example 1; Fig 2; 310pp; English.	
XX	XX	The present sequence encodes a novel protein kinase. The nucleic acids and the protein kinases they encode may be used in the treatment and diagnosis of diseases associated with inappropriate kinase expression such as immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays. The kinase polypeptides may be used as antigens in the production of antibodies of kinase expression and activity. Anti-kinase antibodies and kinase antagonists may also be used to down regulate kinase expression and activity. Diseases related to kinase expression and activity include rheumatoid arthritis, atherosclerosis, autoimmune disorders, complications of organ transplantation, myocardial infarction, immune disorders, cardiomyopathies, strokes, renal failure, oxidative-stress related disorders, chronic inflammatory bowel disease, chronic inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive disorders.	
CC	CC	Sequence 5163 BP; 1336 A; 1352 C; 1266 G; 1207 T; 2 other;	
CC	CC	Query Match: 19.4%; Score 509.4; DB 22; Length 5163;	
CC	CC	Best Local Similarity: 69.4%; Pred. NO. 6.3e-89;	
CC	CC	Matches 706; Conservative 1; Mismatches 307; Indels 3; Gaps 1	
CC	CC	154 ccgcggccagagtcgaagccagcagaagatccctccgggtgggtttttagacatcgaagc 213	
CC	CC	165 cggatggccggcgagcattcgacagcgggcgcggtccgggtgggtcttagacatcgagg 224	
CC	CC	214 ggaacctgggcaaaaggcaacttcgcggtggtggaagctggcgcgcatcgagttaccaaa 273	
CC	CC	225 gacgctggcgcaaggcgcaacttcgcgtgtgtaagcttgggcgcgccagatcaccaga 284	
CC	CC	274 cgcaggttgcatataaataatgtataaacaacgattagattcaagcaatttggagaana 333	
CC	CC	285 cggagggtggcaataaataaatacgaataagcttcagcttgatgcagtgaaccttggagaaa 344	
CC	CC	334 tctatcgttagattcagctgtagaagctcttgaaaccatccacatcatcaaatgaagcttacc 393	
CC	CC	345 tctaccggaagtagtacaataatgtaaaatgtttgaccacacctcacaataatcaacttacc 404	
CC	CC	394 aggttatgaaacaaagacatgctttaaactcgtcatcgaatttggtaaanaatlygagaaa 453	
CC	CC	405 aggtaatggagaccaaagtagtctgtgtacacttgtagcagataatgcaaaaatlygagaaa 464	
CC	CC	454 tgttgattatttgacttccaaacggcgacactgaagttagaagaagcgcggaagaattct 513	
CC	CC	465 tttttgactattcttctaatactgacgggttaaatltagtctgaagcgagaaatct 524	
CC	CC	514 ggcgaatccgtgcggccgtggagactgtagcagaacacatcagctgcacggagactca 573	
CC	CC	525 ggcgaatccgcgtcgtgtgattatgttgcacggtccggaagattgtgcacggtgactcca 584	
CC	CC	574 agacagagaaacctccgtctcgtagtgcgaacatgtagacatacaagcttgcagatttggagtt 633	
CC	CC	585 aagctcgaaatctctcgtcgtgagtaacaacatgatacatacaaatagcagatttcggtttg 644	
CC	CC	634 ggaattctcacagtcagagagcctctgtccacgltgtgtggagagcccccgtatgcg 693	
CC	CC	645 gaattctttaaagatgttgaaactgctgtgcgaacatgctgtgtggcgcccccttaagcag 704	

QY 808 tgcgcagctgagacagcggtgtctgagggcccttcgcacatcccttctcatgtctc 867
 Db 773 tgcgaatctcgcgccgctgtctgagtggaagcttcgcacatcccttctcatgtcca 832
 QY 868 aagactctgagagcctgacccgcgcacatctgtgtgagaccccgcaagcgacaccca 927
 Db 833 cagaatgtgagcatttgacccgcacacatgtgtgtgtagatcccaataagcgccctcca 892
 QY 928 tcgcccagatccgagcagcagcggtgagt 956
 Db 893 tggagcagatctgcagcacaagtgagt 921

RESULT 8

AAFA4655

ID AAF44655 standard; cDNA, 1594 BP.

AC AAF44655;

DT 27-MAR-2001 (first entry)

DE Novel protein kinase cDNA, SEQ ID NO: 35.

KW Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
 KW immunosuppressive; cardiatic; renal; antiinflammatory; antilastmatic;
 KW dermatological; antidiabetic; antifertility; gene therapy; vaccine;
 KW immune disorder; cardiovascular disease; neurodegenerative disease;
 KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;
 KW inflammatory pelvic disease; multiple sclerosis; psoriasis; ss.

XX Mus musculus.

OS WO200073469-A2.

PN 07-DEC-2000.

PF 26-MAY-2000; 2000MO-US14842.

PR 28-MAY-1999; 99US-0136503.

PA (STGE-) SUGEN INC.

PI Plowman GD, Martinez R, Whyte D, Sudersanam S;

DR WPI; 2001-032161/04.

DR P-PSDB; AAB65629.

PT Nucleic acids encoding kinase polypeptides, useful for diagnosing and
 PT treating immune-related diseases and disorders, cardiovascular disease,
 PT neurodegenerative diseases and/or cancers.

XX Disclosure; Fig 2; 310pp; English.

XX The present sequence encodes a novel protein kinase. The nucleic acids
 CC and the protein kinases they encode may be used in the treatment and
 CC diagnosis of diseases associated with inappropriate kinase expression
 CC such as immune-related diseases and disorders, cardiovascular disease,
 CC neurodegenerative diseases and/or cancers. The nucleic acids and
 CC complementary sequences may also be used as DNA probes in diagnostic
 CC assays. The kinase polypeptides may be used as antigens in the production
 CC of antibodies of kinase expression and activity. Anti-kinase antibodies
 CC and kinase antagonists may also be used to down regulate kinase
 CC expression and activity. Diseases related to kinase expression and
 CC activity include rheumatoid arthritis, atherosclerosis, autoimmune
 CC disorders, complications of organ transplantation, myocardial infarction,
 CC immune disorders, cardiomyopathies, strokes, renal failure,
 CC oxidative-stress related disorders, chronic inflammatory bowel disease,
 CC chronic inflammatory pelvic disease, multiple sclerosis, asthma,
 CC osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and
 CC reproductive disorders.

Sequence 1594 BP; 376 A; 488 C; 458 G; 272 T; 0 other;

Query Match

Best Local Similarity 13.18; Score 344; DB 22; Length 1594;
 Matches 509; Conservative 0; Mismatches 275; Indels 0; Gaps 0;

QY 172 gccagcagaagtcctccggtgtgttttagacactcagcagcccttggaagcaagca 231
 Db 62 gccctgaggaacaaccccatgtggcaactatagctgtcctaagcaccatcggaagcgca 121
 QY 232 acttcggtgtgtgagctgtgcggtcatcgaatccacaagaagcgttgcaataaaga 291
 Db 122 acttcgcaaaagtcaagctgtgcgtcatatccctcagccggtgagctgcatataaga 181
 QY 292 taattgataaaacacgatttagattcaagcaatttggagaataatcatatcgttgaagtc 351
 Db 182 tcaattgataaagccacgctggaacccagtaagcttcgagaagcgttccagagaagctccgaa 241
 QY 352 tgaatgaagcttcgaacatccacacatcataaagcttaccaggttatggaacaag 411
 Db 242 ttatgaaggaactcaacccacacatcgtgaagctttagaggtatagaagcgaga 301
 QY 412 acatgcttaccatgctcgaatattgtctaaatgagagaatgtttgatttgaact 471
 Db 302 agacgtataactgtgtgataaatacgtacgacaggaagatgtttgactactcgtgt 361
 QY 472 ccaacgggcaactgtgtagaagcagcgcggaagaagttctggcaatctgtcgccg 531
 Db 362 cgcacggtcgatgaaggaaggaagcgtcgaccaaagttccgcagatcgtgtcagcg 421
 QY 532 tgaagcttaccatgacatccatcgttccacgcggagacccaagcaggaacctctgc 591
 Db 422 tgcactactgtcaccagaagaacatgtacacagggatcttaagagctgaaacctgtgc 481
 QY 592 tggatgtcaacatgagacataagcttgcagatttggatttggaaattcttaagaatcg 651
 Db 482 tggatgcgaagccaacatcaaaatcgcgacttgcgttccagatcgtgtcagctg 541
 QY 652 gagagcctctgtccagctgtgtgtggagcccccgatcgcgcgcgcgaagctttgaag 711
 Db 542 gctcgaagctggaacactctgttggagccccccaacgcgcgcgcgaagctgtccag 601
 QY 712 ggaaggtatgaagcccccaagcttgacatctgagacctgtgtgtgtgtatcgc 771
 Db 602 gcaagaagtatgtaggcagagtgtgacatctgtgagcctgtgtgtatcctgtacaagc 661
 QY 772 tggctcgtgttctcccttcgtagtggcctaactcgcgaagctgtgagacagcggtgc 831
 Db 662 tggtagcggtctccctgccttcgtagtggcacaacctcaagagctgtgtagcgagctcc 721
 QY 832 tgaagggcgcttcgcacatcccttctcatgtctcaagactgtgagagcctgtatcgcc 891
 Db 722 tcagaaggaagtaacggtgtcccttctcatatgtctcaagactgtgagagcctgtcgga 781
 QY 892 gcatgtgtgtgtgagccccgcagcgacatcacatcgcgcagatccggaagcagcggt 951
 Db 782 gattctcgtgtgtgaccccgcaaaacgctgtactgtgagcaaatcatgaagaacaat 841
 QY 952 ggaat 955
 Db 842 ggaat 845

RESULT 9

AAFA4654

ID AAF44654 standard; cDNA; 2190 BP.

AC AAF44654;

DT 27-MAR-2001 (first entry)

DE Novel protein kinase cDNA, SEQ ID NO: 34.

KW Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;

KM immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic;
 KM dermatological; antidiabetic; antiinfertility; gene therapy; vaccine;
 KM immune disorder; cardiovascular disease; neurodegenerative disease;
 KM cancer; autoimmune disorder; stroke; inflammatory bowel disease;
 KM inflammatory pelvic disease; multiple sclerosis; psoriasis; ss.
 OS Homo sapiens.
 XX WO200073469-A2.
 PN 07-DEC-2000.
 XX 26-MAY-2000: 2000MO-US14842.
 PF 28-MAY-1999: 9905-0136503.
 PR (SUGEN-) SUGEN INC.
 PA Plowman GD, Martinez R, Whyte D, Sudersanam S;
 PI WPI; 2001-032161/04.
 DR P-PSDB; AAB65628.
 XX Nucleic acids encoding kinase polypeptides, useful for diagnosing and
 PT treating immune-related diseases and disorders, cardiovascular disease,
 PT neurodegenerative diseases and/or cancers -
 PS Disclosure; Fig 2; 310pp; English.
 XX
 CC The present sequence encodes a novel protein kinase. The nucleic acids
 CC and the protein kinases they encode may be used in the treatment and
 CC diagnosis of diseases associated with inappropriate kinase expression
 CC such as immune-related diseases and disorders, cardiovascular disease,
 CC neurodegenerative diseases and/or cancers. The nucleic acids and
 CC complementary sequences may also be used as DNA probes in diagnostic
 CC assays. The kinase polypeptides may be used as antigens in the production
 CC of antibodies of kinase expression and activity. Anti-kinase antibodies
 CC and kinase antagonists may also be used to down regulate kinase
 CC expression and activity. Diseases related to kinase expression and
 CC activity include rheumatoid arthritis, atherosclerosis, autoimmune
 CC disorders, complications of organ transplantation, myocardial infarction,
 CC immune disorders, cardiomyopathies, strokes, renal failure,
 CC oxidative-stress related disorders, chronic inflammatory bowel disease,
 CC chronic inflammatory pelvic disease, multiple sclerosis, asthma,
 CC osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and
 CC reproductive disorders.
 XX
 SO Sequence 2190 BP; 709 A; 484 C; 504 G; 493 T; 0 other;

Query Match 10.8%; Score 285.4; DB 22; Length 2190;
 Best Local Similarity 61.3%; Pred. No. 6e-46;
 Matches 460; Conservative 0; Mismatches 291; Indels 0; Gaps 0;

QY 216 acccttgagcaaaagcacttcgctggtgagctgagcgagcagcaccacaacg 275
 DB 181 acaatcgagcaaggagacttcgcaaaagtaaatggaagacatccctacagcgaga 240
 QY 276 caggttgcaataaataatgtaaaacagatagatcaagcaacttggaagaatc 335
 DB 241 gaggttgcaataaataatgtaaaacagctgagatcaacaaagctcacaagaatc 300
 QY 336 taccgtgaggttcagctgagagcttcgtaacacatcacacataaagcttaccag 395
 DB 301 ttcagagaaagtaagaataagatttaatacatcccaatagagaagtattcgaa 360
 QY 396 gtaatggaacaagaagcacttcacatgctacacgaattgtctaataatgagaatg 455
 DB 361 gtaatggaacaagtaaaacacatccacatcaatggaataatgagagtgaa 420
 QY 456 ttgatattcttcacagcgacccctgagtgagagcagcgaggaagcttcgg 515
 DB 421 ttgacatttggctgacactggcagagatgaaagaaagcaagacataatctaga 480

QY 516 caatctctgcgcgtgagagctactgtcacagacatcacatcgtccacgagacccaag 575
 DB 481 cagatttgctgcagctacatcactgcacagaagaagatcgatcacatcgagacccaag 540
 QY 576 accgagacccctccgctgagctgcaacatgacatcgaagcttgccagatttgattggg 635
 DB 541 gctgaataatctattgttagatgcagatagaacataaataagatgattcgatttagc 600
 QY 636 aattctacaagtcagagagccctcgtccacgtggtgtggaagccccgtatgcccgc 695
 DB 601 aatgaattactgttgcgcgttaactgcagacgcttcttgagcagctccatcaagcaga 660
 QY 696 ccggaagctcttgagggagagatgaagggccccagcttgagacatctgagcctgggc 755
 DB 661 cctgagctctccagagcaagaataatgacgagccagaagtgatgtgtgagcttgagg 720
 QY 756 gtggtgtgagctgcgcgtgcgttcctcccttcgattgagggcctaaccctgcagag 815
 DB 721 gtaatttaacaacactagctcagtgctcacttccttgatgaggaacaaactaaagaa 780
 QY 816 ctgagacagcggtgctgagagggccgcttcgcacatccctctcatgtctcaagactgt 875
 DB 781 ctgagagagagagatgaagaagaaatacagaatctccctctacatgcttaagactgt 840
 QY 876 gagagcttgatccgcgcgactgtgtgtgtgagcccgccagagcgaatccatccagc 935
 DB 841 gaaaccttcacaacgcttcctgtgtctaataatcaatcaacgagcagcacttagagcaa 900
 QY 936 atccgagcagcagcggtgagtgagcggtcagc 966
 DB 901 atcatgaagagcaggtgagatcaatgagcaggc 931

RESULT 10
 AAV03002
 ID AAV03002 standard; cDNA to mRNA; 2698 BP.
 AC AAV03002;
 XX
 XX 18-JUN-1998 (first entry)
 DE Human Twenty-five C associated protein kinase 1 encoding cDNA.
 KW Human; twenty-five C associated protein kinase 1; TCAK1; detection;
 KW cancer; cell proliferation; Cdc25; phosphorylation; 14-3-3 protein; ds.
 XX
 OS Homo sapiens.
 XX
 XX
 FH Key Location/Qualifiers
 FT CDS 376..2565
 FT /*tag= a
 FT /product= "TCAK1"
 XX
 XX
 PN WO9801756-A1.
 PD 15-JAN-1998
 PF 03-JUL-1997: 97MO-US11721.
 XX
 PR 09-JUL-1996: 96US-0677298.
 XX
 PA (UNIW) UNIV WASHINGTON.
 PI P1wnica-Worms H;
 XX
 DR WPI: 1998-101198/09.
 DR P-PSDB; AAB37158.
 XX
 PT DNA encoding Twenty-five C Associated protein Kinase 1 - useful for,
 PT e.g. detecting cancers or disorders of cell proliferation
 XX
 PS Claim 2; Page 35-39; 75pp; English.

SQ Sequence 3857 BP; 1126 A; 991 C; 920 G; 820 T; 0 other;

Query Match	10.6%	Score 279.2;	DB 22;	Length 385/;
Best Local Similarity	60.6%;	Pred. NO. 1e-44;		
Matches 458; Conservative	0;	Mismatches 298;	Indels 0;	Gaps 0;

[illegible]

RESULT 12
AAf85149
ID AAF85149 standard; DNA; 4790 BP.
XX
AC AAF85149;
XX
DT 09-JUL-2001 (first entry)
XX
DE DNA encoding a disveilled associated kinase (DAK) isoform DAKb.
XX
KW Disveilled associated kinase; DAK; DAKa; DAKb; DAKc; cell proliferation;
KM cancer; ss.
XX

OS Homo sapiens.

aa	Key	Location/Qualifiers
FH		

CDS
ET
ET

FT	EM	product-	disvelled	associated	kinase (DAK)	isoform
			DAK ^h			

PN WO200125408-A1

AA 12-APR-2001
PD

XX
PF 06-OCT-2000: 2000MO-US27899.

XX 06-OCT-1999. 99115-0158021

PR 14-SEP-2000; 2000US-0661965.

PA (REGC) UNIV. CALIFORNIA

XX
PI Sun T, Williams LT:

XX WPB : 2001-316169/33
DP

DR P-PSDB; AAB68341.

Novel isolated Dishevelled associated kinase polypeptide which

PT phosphorylates Dishevelled polypeptides, useful in screening assays to identify compounds for treating cancers by modulating kinase activity

PT
yy

PS Claim 10; Fig 10A-B; 93pp; English.

Sequence 4790 BP; 1519 A; 1179 C; 1078 G; 1014 T; 0 other

Query Match	10.6%	Score 279.2	DB 22	Length 4790
Best Local Similarity	60.6%	Pred. No. 1.1e-44		
Matches 458; Conservative		0; Mismatches 298	Indels 0	Gaps 0

QY 201 taagacatcgagcgagaccggcggaagaggaacttcgsggtgtgaagcttgccgagcat 260
 Db 1618 tacaacattcaataagaagatctcggaagggaaattctgcgaagtgtaactaagcgaataac 1677
 QY 261 cgagtcaccaaaagaacgaggtctgcatabaaataattgataaaacagactatgaattcaagc 320
 Db 1678 ctgcgcattgccaaggggtctgcgcataagaataattgacaagaagcccaactcaactctg 1737
 QY 321 aatttgagaataatctatcgctgaggttcagctcytaagagcttcgaacatccacaatc 380
 Db 1738 tcactacagaaactctttagagaggttagaataatgaatgctgtgatacccaacata 1797
 QY 381 ataaagctttccaggttatgagaacaaagacatcgtcttaacatcgctcaatattcgt 440
 Db 1798 gtaaatgtttccagaaataatcogaagaacggaagacgctctatctgactctgagtaagca 1855


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Db 1681 aggtctagggggttgaggagctgtctgtccctgtcagcttccagagaggaagcgc 1740
Oy 1741 gggcgctcgacacctcaactcaactaagggctgaagccttcggcagcagctgaaga 1800
Db 1741 gggcgctcgacacctcaactcaactaagggctgaagccttcggcagcagctgaaga 1800
Oy 1801 ccccgaggaacaaagggttcttggtactgaacaaatcaagggtgtgtctgcaggtgtc 1860
Db 1801 ccccgaggaacaaagggttcttggtactgaacaaatcaagggtgtgtctgcaggtgtc 1860
Oy 1861 gcaaggtcccttcgacggcgccagcaggggcgccgagcccttcacagcccttcac 1920
Db 1861 gcaaggtcccttcgacggcgccagcaggggcgccgagcccttcacagcccttcac 1920
Oy 1921 agagcccaaggccttcgacggcgccagcaggggcgccgagggcttgagcccttcgag 1980
Db 1921 agagcccaaggccttcgacggcgccagcaggggcgccgagggcttgagcccttcgag 1980
Oy 1981 aggtgtcagaagcagaagctgtctcagttacagacacacccggcgctgcagccgct 2040
Db 1981 aggtgtcagaagcagaagctgtctcagttacagacacacccggcgctgcagccgct 2040
Oy 2041 gctccagagcccccagcggcccttcgcccgtttgtatgcgcccctgtgatgcccctg 2100
Db 2041 gctccagagcccccagcggcccttcgcccgtttgtatgcgcccctgtgatgcccctg 2100
Oy 2101 gggcgctccgctcccccagacccctctcagctgcggggctcccgctgtgcgcccac 2160
Db 2101 gggcgctccgctcccccagacccctctcagctgcggggctcccgctgtgcgcccac 2160
Oy 2161 tctctgagagcggcgcttcccccgttgctcctcagcggcgccagctctctgacacacactgc 2220
Db 2161 tctctgagagcggcgcttcccccgttgctcctcagcggcgccagctctctgacacacactgc 2220
Oy 2221 acattgacacggcgcccccagcggcccttcgcccgtgtgcccacacagcggctgcgagctgc 2280
Db 2221 acattgacacggcgcccccagcggcccttcgcccgtgtgcccacacagcggctgcgagctgc 2280
Oy 2281 ccccgaggttgagcccttcggtgctgtcagagggaactgtagaatgagagcctgtatgc 2340
Db 2281 ccccgaggttgagcccttcggtgctgtcagagggaactgtagaatgagagcctgtatgc 2340
Oy 2341 cctgtctccagagcgtttgtcctgtgtgagtgagggcgccctgtatcctgtgcagga 2400
Db 2341 cctgtctccagagcgtttgtcctgtgtgagtgagggcgccctgtatcctgtgcagga 2400
Oy 2401 cactgactcttacagcaataactcaagagagtgagacaatctgcgtcaaaccaaga 2460
Db 2401 cactgactcttacagcaataactcaagagagtgagacaatctgcgtcaaaccaaga 2460
Oy 2461 acttctagaagcgaataaagcaatacgttaggtgttttgcgcaaaaaaaaaaaaaa 2520
Db 2461 acttctagaagcgaataaagcaatacgttaggtgttttgcgcaaaaaaaaaaaaaa 2520
Oy 2521 aaaaaaaaaaaaaa 2533
Db 2521 aaaaaaaaaaaaaa 2533

RESULT 2
AAx82952 standard; cDNA; 2632 BP.
ID AAx82952 standard; cDNA; 2632 BP.
AC AAx82952;
XX
XX 07-JUL-2000 (first entry)
XX
XX Human keratinocyte derived pKex122 encoding cDNA #2.
XX
XX Keratinocyte: regulatory protein: human: pKex122; antiproliferative;
XX kinase; signal transduction; desmosome; dermatological condition;
XX pemphigus vulgaris; psoriasis vulgaris; epidermis; cosmetic; SS.
XX
```

```
OS Homo sapiens.
XX
XX WO200017232-A2.
XX
XX 30-MAR-2000.
XX
XX 06-SEP-1999; 99NO-DE02865.
XX
XX 19-SEP-1998; 98DE-1042863.
XX
XX (KRAM/) KRAMER M.
XX
XX Kramer M, Bechtel M, Reinartz J, Schaefer B, Wallich R;
XX WPI: 2000-283542/24.
XX
XX P-PSDB: AAM90879.
XX
XX New regulatory polypeptide from keratinocytes, useful for diagnosis and
XX treatment of dermatological disorders, also in cosmetics
XX
XX Claim 2; Page 55; 55pp; German.
XX
XX This invention describes a novel human regulatory polypeptide designated
XX pKex122 (I), or its variants from human keratinocytes, which in activated
XX keratinocytes is the same as, or similar to, the most highly expressed
XX protein and has antiproliferative activity. (I) is a kinase involved in
XX signal transduction and is conjectured to be involved in cell-cell or
XX cell-matrix interactions and/or formation of (hemi)desmosomes. Modulation
XX of (I) will affect proliferation and differentiation of keratinocytes.
XX (I) is upregulated in some dermatological conditions, e.g. pemphigus
XX vulgaris and psoriasis vulgaris. (I) is used to raise specific antibodies
XX (Ab) which are used for diagnosis and treatment of dermatological
XX disorders and for cosmetic treatment of the epidermis. Nucleic acid (II)
XX that encodes (I) is used: (i) to produce transgenic mammals (particularly
XX mice and rats); and (ii) as source of sense and antisense
XX oligonucleotides for diagnosis and treatment of dermatological disorders
XX and for cosmetic treatment of the epidermis. (II), (I) and polypeptides
XX (Ia) produced by splice variants of (II) are used to identify specific
XX binding agents (potentially useful in medicine and cosmetics) that
XX modulate their function and/or expression, especially inhibitors and
XX activators. Cells and animals transformed with (II) are used to study
XX (i)-induced changes in cell morphology and basic functions. This
XX sequence encodes the human keratinocyte protein pKex122 described in the
XX method of the invention.
XX
XX Sequence 2632 BP: 513 A; 852 C; 809 G; 458 T; 0 other:
XX
XX Query Match 99.6%; Score 2522.8; DB 21; Length 2632;
XX Best Local Similarity 99.9%; Pred. No. 0;
XX Matches 2524; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX Oy 8 aggtgcgagcagcagatggtatcatgtcggaggttcagcgccgagcccgggcagag 67
XX 107 aggtgcgagcagcagatggtatcatgtcggaggttcagcgccgagcccgggcagag 166
XX Oy 68 tcaaggcagcagagcccttcggtgtgttttctacagacatcgagcggagccttggcga 127
XX 167 tcaaggcagcagagcccttcggtgtgttttctacagacatcgagcggagccttggcga 226
XX Oy 128 aggcacttcggtgtgtgtgaagctgcgagcagcagatcccaaaacgaggttgcgaat 187
XX 167 tcaaggcagcagagcccttcggtgtgttttctacagacatcgagcggagccttggcgaat 286
XX Oy 188 aaaaataatgataaacaacagatagattcaagcaatttggagaaaaatctatctggagt 247
XX 287 aaaaataatgataaacaacagatagattcaagcaatttggagaaaaatctatctggagt 346
XX Oy 248 tcaagctgatgaagcttctgaacacatcacacatataaagctttacaggtttatgaaac 307
XX 347 tcaagctgatgaagcttctgaacacatcacacatataaagctttacaggtttatgaaac 406
XX Oy 308 aagagacatgcttatacatgctcactgaattgtctaaataatgagagaatgtttgatattc 367
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|||||
Db 407 aaagacatgcttcaacacgacacgttgcataaataaggagaaagtgttatatt 466
QY 368 gacttccaaacggcaccctgtagtgaagacgagcgagaaagtctgycaaatctgtc 427
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Db 467 gacttccaaacggcaccctgtagtgaagacgagcgagaaagtctgycaaatctgtc 526
QY 428 ggcgctgtagtactctgtaacagacatacatgccaacggagacccccaagaccgaaacct 487
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Db 527 ggcgctgtagtactctgtaacagacatacatgccaacggagacccccaagaccgaaacct 586
QY 488 cctgtgtgtagtgcacaacatgagacatacaagctggcagatttgatttggaaatttcaaa 547
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Db 587 cctgtgtgtagtgcacaacatgagacatacaagctggcagatttgatttggaaatttcaaa 646
QY 548 gtaagagagacctctgtccacgtggtgtgagagcccccgtatgacgcccggaaagtctt 607
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Db 647 gtaagagagacctctgtccacgtggtgtgagagcccccgtatgacgcccggaaagtctt 706
QY 608 tgaagagagagtagtgaagagccccaagtgaacatactgtagacctgggctgtgtcta 667
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Db 707 tgaagagagagtagtgaagagccccaagtgaacatactgtagacctgggctgtgtcta 766
QY 668 cgtccctgtctgcggttctctccctccctccatgtaggacataccctgacagctgtagacag 727
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Db 767 cgtccctgtctgcggttctctccctccctccatgtaggacataccctgacagctgtagacag 826
QY 728 ggtgtctgtagagcgagcttccatccctcttcatgttcaagaactgtgaagacctgat 787
|||||
Db 827 ggtgtctgtagagcgagcttccatccctcttcatgttcaagaactgtgaagacctgat 886
QY 788 ccgacccagctgtagtgaagcccgacagcgacatacaatcgcgccaatcccgacaga 847
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Db 887 ccgacccagctgtagtgaagcccgacagcgacatacaatcgcgccaatcccgacaga 946
QY 848 ccggtgtagtgcggtctgtagacccctgtgacggagaccccgacccgaccttccgcagaca 907
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Db 947 ccggtgtagtgcggtctgtagacccctgtgacggagaccccgacccgaccttccgcagaca 1006
QY 908 caggtctacaactccaaactctggcgactagatgaagacgagctgggtgtatcatgacaacct 967
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Db 1007 caggtctacaactccaaactctggcgactagatgaagacgagctgggtgtatcatgacaacct 1066
QY 968 ggcgctgtagacccgacagagacggtgtagatcaactgtgcacaaacagacatacaacctgtgc 1027
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Db 1067 ggcgctgtagacccgacagagacggtgtagatcaactgtgcacaaacagacatacaacctgtgc 1126
QY 1028 tgcacatttaactcctccttgcagcgctcaagagatctcggaatgcccagctgcgcgcg 1087
|||||
Db 1127 tgcacatttaactcctccttgcagcgctcaagagatctcggaatgcccagctgcgcgcg 1186
QY 1088 ccccgagcctctgcagagacagccgagctgcgagctgcgagcctccagatggtcttggaggtgac 1147
|||||
Db 1187 ccccgagcctctgcagagacagccgagctgcgagctgcgagcctccagatggtcttggaggtgac 1246
QY 1148 tcagagagagtgctttcacacgagaccccttcacgacctgctgtgtgcacgacagcgagagac 1207
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Db 1247 tcagagagagtgctttcacacgagaccccttcacgacctgctgtgtgtgcacgacgagagac 1306
QY 1208 ctgtgtgtagtctgcgttccatcagacgagatgtagctgtgagctccagagctctgtcaggt 1267
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Db 1307 ctgtgtgtagtctgcgttccatcagacgagatgtagctgtgagctccagagctctgtcaggt 1366
QY 1268 ggcctgtgtcttcacggtgtagtgcagctgtgcagcgagatggttccgagcccgagccgtgtc 1327
|||||
Db 1367 ggcctgtgtcttcacggtgtagtgcagctgtgcagcgagatggttccgagcccgagccgtgtc 1426
QY 1328 cccaagcagcctgtgtagacagccaatcagtgaagagcgacagggccagggcccgagcctaga 1387
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Db 1427 cccaagcagcctgtgtagacagccaatcagtgaagagcgacagggccagggcccgagcctaga 1486
QY 1388 ggaagagcagagacagcagagagtcctctgcacagcagacagggccgagagcacaacctgtgc 1447
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Db 1487 ggaagagcagagacagcagagagtcctctgcacagcagcgagcgagacacacctgtgc 1546
QY 1448 cgaaggtctcacccgctcttcccaactcacccgacatgtatagtgtgtcccccctcac 1507
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Db 1547 cgaaggtctcacccgctcttcccaactcacccgacatgtatagtgtgtgtcccccctcac 1606
QY 1508 caagcagagctctgtagagaggaacagactctgtagactgtgtgacatctctctctgcagacaa 1567
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Db 1607 caagcagagctctgtagagaggaacagactctgtagactgtgtgacatctctctctgcagacaa 1666
QY 1568 aagcccgcgaggtctgtagaccccgacactcaagggctgtgtgcgctgtctccc 1627
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QY 1628 ggtgaagctgtgacccctgcgagcttccctggggtgcagatccgcaaccccaagtgtctgcagaccta 1687
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Db 1727 ggtcaagctgtgacccctgcgagcttccctggggtgcagatccgcaaccccaagtgtctgcagaccta 1786
QY 1688 ggggagcttggagagagctgtctctgcctcctgtcaagcttccagagagggagcgcgctgc 1747
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Db 1787 ggggagcttggagagagctgtctctgcctcctgtcaagcttccagagagggagcgcgctgc 1846
QY 1748 ggaacactcaactgactcaagggctggaagaccttccgagcagctgtgtagagacacagcg 1807
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Db 1847 ggaacactcaactgactcaagggctggaagaccttccgagcagctgtgtagagacacagcg 1906
QY 1808 gaccaaaaggtgttctgtagactggaacaaatcaaggggctgtgctgcagagtgtgtccaggt 1867
|||||
Db 1907 gaccaaaaggtgttctgtagactggaacaaatcaaggggctgtgctgcagagtgtgtccaggt 1966
QY 1868 cccctgacagccgggacagagggcgagctgtagcccttccacgacccctgcacagagacc 1927
|||||
Db 1967 cccctgacagccgggacagagggcgagctgtagcccttccacgacccctgcacagagacc 2026
QY 1928 aggcctgtagcggcgagcagacccgacagcgagggagggctgtgcagagaggtgtct 1987
|||||
Db 2027 aggcctgtagcggcgagcagacccgacagcgagggagggctgtgcagagaggtgtct 2086
QY 1988 aagacagcagagagctgtctccagcttcaagacacacccggcgctgacacccggctgtccca 2047
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Db 2087 aagacagcagagagctgtctccagcttcaagacacacccggcgctgacacccggctgtccca 2146
QY 2048 ggcacccacagccggcctgtgcacgcttgtgtatgcgccccctgtgtagtgccttgggctgtgc 2107
|||||
Db 2147 ggcacccacagccggcctgtgcacgcttgtgtatgcgccccctgtgtagtgccttgggctgtgc 2206
QY 2108 cccggttccacagacacccctcccaacgctgcgagctcccgctgtctgcgcgccccacactgtga 2167
Db 2207 cccggttccacagacacccctcccaacgctgcgagctcccgctgtctgcgcgccccacactgtga 2266
QY 2168 gacccgagcgttcccccgtgtgcctcagcgagctccctgtgacacacacactgtgacatgtg 2227
|||||
Db 2267 gacccgagcgttcccccgtgtgcctcagcgagctccctgtgacacacacactgtgacatgtg 2326
QY 2228 caacggccccacagcctcctcccgctgtgcctcccaacagcctgtgcgagctgtgcgccccag 2287
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QY 2288 ttgtgagccccctggggctgtgcagggagactgtgaga ttgagagcctgtatgtccctgtc 2347
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Db 2387 ttgtgagccccctggggctgtgcagggagactgtgaga ttgagagcctgtatgtccctgtc 2446
QY 2348 cctaagcagcttctgtctgtgtagtgaaggagacccctgtacatctctgtgcagagacatgtac 2407
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Db 2447 cctaagcagcttctgtctgtgtagtgaaggagacccctgtacatctctgtgcagagacatgtac 2506
QY 2408 tcttaagcaataacttcaagagaggtgaagacatctgtgccttcaagccaagcaacttct 2467
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Db 2507 tcttaagcaataacttcaagagaggtgaagacatctgtgccttcaagccaagcaacttct 2566
QY 2468 agaagcgaataaagcaataacgtttaagtgcttctgtgcgaataaataaataaataaataa 2527
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Db 2567 agaagcgaataaagcaataacgtttaagtgcttctgtgcgaataaataaataaataaataa 2626


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Oy 906 cacagctaacctcaactcctgctgagctacgtatgacgagctggtatcatatgcaagcc 965
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Db 61 cacagctaacctcaactcctgctgagctacgtatgacgagctggtatcatatgcaagcc 120
Oy 966 ctggagctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1025
    |||||||
Db 121 ctggagctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180
Oy 1026 gctgcattatatactcctcctctgagcagcagcagcagcagcagcagcagcagcagc 1085
    |||||||
Db 181 gctgcattatatactcctcctctgagcagcagcagcagcagcagcagcagcagcagcagc 240
Oy 1086 cgcgccgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1145
    |||||||
Db 241 cgcgccgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 300
Oy 1146 cctcaggaagctcttccacagcagcagcagcagcagcagcagcagcagcagcagcagc 1205
    |||||||
Db 301 cctcaggaagctcttccacagcagcagcagcagcagcagcagcagcagcagcagcagc 360
Oy 1206 acctgtgtcagctcgtcctcctcagcagcagcagcagcagcagcagcagcagcagcagc 1265
    |||||||
Db 361 acctgtgtcagctcgtcctcctcagcagcagcagcagcagcagcagcagcagcagcagc 420
Oy 1266 tggccctgtgtcctcctcctcagcagcagcagcagcagcagcagcagcagcagcagc 1325
    |||||||
Db 421 tggccctgtgtcctcctcctcagcagcagcagcagcagcagcagcagcagcagcagc 480
Oy 1326 tccccaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1385
    |||||||
Db 481 tccccaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 540
Oy 1386 gagagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1445
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Db 541 gagagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 600
Oy 1446 ggcgaagcttccacagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1484
    |||||||
Db 601 ggcgaagcttccacagcagcagcagcagcagcagcagcagcagcagcagcagcagc 639

RESULT 5
AAF44658
ID AAF44658 standard; cDNA; 5163 BP.
XX
AC AAF44658;
XX
DT 27-MAR-2001 (first entry)
XX
DE Novel protein kinase cDNA, SEQ ID NO: 38.
XX
KW Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
KW immunosuppressive; cardiac; renal; antiinflammatory; antiasthmatic;
KW metabolic; antidiabetic; antifertility; gene therapy; vaccine;
KW immune disorder; cardiovascular disease; neurodegenerative disease;
KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;
KW inflammatory pelvic disease; multiple sclerosis; psoriasis; ss.
OS Homo sapiens.
XX
PN WO200073469-A2.
XX
PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000MO-US14842.
XX
PR 28-MAY-1999; 99US-0136503.
XX
PA (SUGR-) SUGEN INC.
XX
PI Plowman GD, Martinez R, Whyte D, Sudersanam S;
XX
```

```
DR WPI: 2001-032161/04.
DR P-PSDB: AAB65631.
XX
PT Nucleic acids encoding kinase polypeptides, useful for diagnosing and
PT treating immune-related diseases and disorders, cardiovascular disease,
PT neurodegenerative diseases and/or cancers -
XX
PS Example 1; Fig 2; 310pp; English.
XX
CC The present sequence encodes a novel protein kinase. The nucleic acids
CC and the protein kinases they encode may be used in the treatment and
CC diagnosis of diseases associated with inappropriate kinase expression
CC such as immune-related diseases and disorders, cardiovascular disease,
CC neurodegenerative diseases and/or cancers. The nucleic acids and
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays. The kinase polypeptides may be used as antigens in the production
CC of antibodies of kinase expression and activity. Anti-kinase antibodies
CC and kinase antagonists may also be used to down regulate kinase
CC expression and activity. Diseases related to kinase expression and
CC activity include rheumatoid arthritis, atherosclerosis, autoimmune
CC disorders, complications of organ transplantation, myocardial infarction,
CC immune disorders, cardiomyopathies, strokes, renal failure,
CC oxidative-stress related disorders, chronic inflammatory bowel disease,
CC chronic inflammatory pelvic disease, multiple sclerosis, asthma,
CC osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and
CC reproductive disorders.
XX
SQ Sequence 5163 BP; 1336 A; 1352 C; 1266 G; 1207 T; 2 other;

Query Match 20.28; Score 511; DB 22; Length 5163;
Best Local Similarity 69.58; Pred. No. 7.5e-91;
Matches 707; Conservative 1; Mismatches 306; Indels 3; Gaps 1;

Oy 55 ccgagggcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 114
    || |||| || || |||| || || |||| || || |||| || || |||| || || |||| ||
Db 165 cggatgcccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 224
Oy 115 ggaacctgggcaaaagcaacttcgcggtgtgaaagctgagcagcagcagcagcagcagc 174
    || |||| || || |||| || || |||| || || |||| || || |||| || || |||| ||
Db 225 gcaagctgggcaaaagcaacttcgcggtgtgaaagctgagcagcagcagcagcagcagc 284
Oy 175 cgcaggtgtgcaataaataatgataaacaagcagcagcagcagcagcagcagcagcagc 234
    || |||| || || |||| || || |||| || || |||| || || |||| || || |||| ||
Db 285 cggaggtgtgcaataaataatgataaacaagcagcagcagcagcagcagcagcagcagc 344
Oy 235 tctatcgtgaagctcagctgtaagcttcgaacacacacacacacacacacacacacacac 294
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Db 345 tctatcggagaagctcacaataatgataaagctgagccacccacacacacacacacacac 404
Oy 295 aggtatggaacaagaagacatgcttaccatgcgtcactgaaattgctaaataatgagaaa 354
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Db 405 aggtatggaacaagaagacatgcttaccatgcgtcactgaaattgctaaataatgagaaa 464
Oy 355 tgtttgattattgacttccaaacagcgccagtgatggaagagcgcgaggaagtctct 414
    || || || || || || || || || || || || || || || || || || || || || || ||
Db 465 ttttgatactctgtcaatacatatgagccggttaaatgagctgaaagcagcgaaatactc 524
Oy 415 ggcacatcctgtcgccgtgagctgtcagcagcagcagcagcagcagcagcagcagcagcagc 474
    || || || || || || || || || || || || || || || || || || || || || || ||
Db 525 ggcacatcctgtcgccgtgagctgtcagcagcagcagcagcagcagcagcagcagcagcagc 584
Oy 475 agaccgagaacctcctcgtgagtgagcaacatgagcagcagcagcagcagcagcagcagc 534
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Db 585 aagctgaaaatctcctcgtgatacaacaatgaaataaataagcagattcgtgtttg 644
Oy 535 ggaattcttaagaagtgagagcctgttcacagtggtggtgagagcccccgtatccg 594
    || || || || || || || || || || || || || || || || || || || || || || ||
Db 645 gaaattcttaagaagtgagagcctgttcacagtggtggtgagagcccccgtatccg 704
Oy 595 ccccggaagcttctgagggaggaagatgagagcccccagcagcagcagcagcagcagcagc 654
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Db 705 ccccggaagcttctgagggaggaagatgagagcccccagcagcagcagcagcagcagcagc 764
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KM Inflammatory pelvic disease; multiple sclerosis; psoriasis; ss.
 XX Homo sapiens.
 OS
 XX WO200073469-A2.
 PN
 XX 07-DEC-2000.
 PD
 XX 26-MAY-2000; 2000MO-US14842.
 PF
 XX 28-MAY-1999; 99US-0136503.
 PR
 XX (SUGF-) SUGEN INC.
 PA
 XX Plowman GD, Martinez R, Whyte D, Sudersanam S;
 PI
 DR MPI: 2001-0312161/04.
 XX P-PSDB; AAB65628.
 DR
 XX
 XX
 PT Nucleic acids encoding kinase polypeptides, useful for diagnosing and
 PT treating immune-related diseases and disorders, cardiovascular disease,
 PT neurodegenerative diseases and/or cancers -
 PS
 XX Disclosure; Fig 2; 310pp; English.
 XX
 CC The present sequence encodes a novel protein kinase. The nucleic acids
 CC and the protein kinases they encode may be used in the treatment and
 CC diagnosis of diseases associated with inappropriate kinase expression
 CC such as immune-related diseases and disorders, cardiovascular disease,
 CC neurodegenerative diseases and/or cancers. The nucleic acids and
 CC complementary sequences may also be used as DNA probes in diagnostic
 CC assays. The kinase polypeptides may be used as antigens in the production
 CC of antibodies of kinase expression and activity. Anti-kinase antibodies
 CC and kinase antagonists may also be used to down regulate kinase
 CC expression and activity. Diseases related to kinase expression and
 CC activity include rheumatoid arthritis, atherosclerosis, autoimmune
 CC disorders, complications of organ transplantation, myocardial infarction,
 CC immune disorders, cardiomyopathies, strokes, renal failure,
 CC oxidative-stress related disorders, chronic inflammatory bowel disease,
 CC chronic inflammatory pelvic disease, multiple sclerosis, asthma,
 CC osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and
 CC reproductive disorders.
 CC
 XX
 SO Sequence 2190 BP; 709 A; 484 C; 504 G; 493 T; 0 other;

Query Match 11.3%; Score 285.4; DB 22; Length 2190;
 Best Local Similarity 61.3%; Pred. No. 7.8e-47;
 Matches 460; Conservative 0; Mismatches 291; Indels 0; Gaps 0;

QY 117 accctgggcaaaagcaacttcggtggtgaagctggcgcgatcgagtcacccaacg 176
 II I IIIII
 DB 181 acaatcgcaagggaatttgcacaagtaaatgtgcaagatattccttaacgagga 240
 QY 177 caggttgcaataaataatgtataaacacgattagattcgaacttgggagaaatc 236
 I
 DB 241 gaagttgcataaataatgtacaacacgcagttgaatccaacagttcacaagaatc 300
 QY 237 taccgtgaagttcagcgtgaagcttcgaaccatccacacatcatcaaaagctttaccg 296
 I
 DB 301 ttcagagaagtaagaataagaagattttaacatccatccaatatagtgaaagttattcgaa 360
 QY 297 gttatggaaacaaagacatgcttaccatcgctacgtgaatttgcataaaatcgagaatg 356
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 DB 361 gtcattgaacactgaaaaaacacttacctatcatgtgaatagtgagtggaagta 420
 QY 357 ttgattatattgacttccaaaggacactgagtgagaagcgcgcggaagattctg 416
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 DB 421 ttgactatttggctcacatggcagagtgaaagaaagaacgaatcctaattaga 480
 QY 417 caaatccgtcgccggtggaggtactgtcagacatcaatcgtcccgggagcttaag 476
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 DB 481 cagattgtgtcgtcaggttcacatctgcacacccaagaacgagtcgtacacgagactcaag 540

QY 477 accgagaacctcctcgtgatgcaacatgacatcaagctggcagaatttgattggg 536
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 QY 537 aatttcaacagtcagagagcctctgtccacgtggtgtgtggagcccccgatagccg 596
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 DB 601 aattgaattactgttgcgtglaaacctgcgacagcttctgtgacgttccctcaccagca 660
 QY 597 ccggaagctcttgagggaaggagatgaaggcccccagctggacatctggaacctgggc 656
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 DB 661 cctgagctctccagggcaagaataatagacggccagaagtgtgattgtgtctgggg 720
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 DB 721 gtcatttatacacacactagtcagtgctcacttccctttagtggtgcaaaacctaaaggaa 780
 QY 717 ctgagacagcgggtgtcgtggggccgcttcgcgatccctcttcatggtcgaagactgt 776
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 DB 781 ctgagagagagagatataagaaggaaatcacagaattccctctcactgactacagactgt 840
 QY 777 gagagcctgattccgcgcgatgtgtgtgaccgccgcagcgcatcacatcgccag 836
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 DB 841 gaaaccttctcaaacgtttccctcgtgtctaattccaattaaacgctgactcagagcaa 900
 QY 837 atccgcagcaccggtgagatcggtcgtgagc 867
 I
 DB 901 atcattgaagcagcaggtgattcaatgacagggc 931

RESULT 10
 AAV03002
 ID AAV03002 standard; cDNA to mRNA; 2698 BP.
 AC
 XX AAV03002;
 XX
 DF 18-JUN-1998 (first entry)
 XX
 XX Human Twenty-five C associated protein kinase 1 encoding cDNA.
 XX
 KM Human; twenty-five C associated protein kinase 1; TcAK1; detection;
 KM cancer; cell proliferation; Cdc25; phosphorylation; 14-3-3 protein; ds.
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 OS Homo sapiens.
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 FH Key Location/Qualifiers
 FT CDS 376..2565
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 FT /product- "TcAK1"
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 PN MO9801756-A1.
 PN
 XX
 PD 15-JAN-1998.
 PD
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 PF 03-JUL-1997; 97MO-US11721.
 PF
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 PR 09-JUL-1996; 96US-0677298.
 PR
 XX
 PA (UNIW) UNIV WASHINGTON.
 PA
 XX
 PI Plwica-Worms H;
 PI
 DR MPI: 1998-101198/09.
 DR
 XX
 DR P-PSDB; AAW37158.
 DR
 XX
 PT DNA encoding Twenty-five C Associated protein kinase 1 - useful for,
 PT e.g. detecting cancers or disorders of cell proliferation
 PT
 XX
 PS Claim 2; Page 35-39; 75pp; English.
 PS
 CC The present sequence encodes human twenty-five C associated protein
 CC kinase 1 (TcAK1). The present invention also describes: creating a
 CC 14-3-3 recognition motif within a TcAK1 substrate by incubating the

	Best Local Similarity	60.6%	Pred. No. 1.4e-45;	
	Matches 458; Conservative	0;	Mismatches 298; Indels	0; Gaps
OY	102	tacgacatcgcgagcccgcttggcaaaaggacaacttcgcgtgttgtaagcttggcgcgcgat	161	
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OY	162	cgaatcaccaaaaacgcaggtctgcaaataaabaatlgtataaaacagatatagattcaagc	221	
Db	1736	ctgcaccaatcgcgaagaggtctgcacataagataattgttcaaaagaccacctcaatccttgg	1795	
OY	222	aatttgggaaaaatttatctcgttaggtttcaagcttgatgaagcttcttgaaccatccacatc	281	
Db	1796	tcaactaccegaaactctttagagaggttttgaataaagaatgtctgtatcacccccacata	1855	
OY	282	ataaagctttccaggttatitgaaaacaaggacatgctttatactgtcatactaatcttcct	341	
Db	1856	gttaaattgttcccgaagtatacgaaaacggaagaagacgctctatctyatatactgagtacga	1915	
OY	342	aaaaatggagaanaatgtttgatatttgtacttccaaacggcgacacttgatgagaacagcg	401	
Db	1916	tctggcggagaagatcttctgactactgtttctccacgagcagatgaagaagagaagcg	1975	
OY	402	cggaaagagctctgycgaatactctgcgcgcgttgagatctgttcaacacatcacatcgttc	461	
Db	1976	cgaattgaagtttctgcgaatatcgttccacgcgtgacatattgttcalcaaaaagaataatt	2035	
OY	462	caccgggacccccaagaccgagaaactctctgtcgttggatgtgcaaatgtgacatcagcttgc	521	
Db	2036	cacaaaggacttaaaagccgaaaaccttctgtcgtgcacgagaaactgtaaatcacaatcgc	2095	
OY	522	gattttgattcttgggaattcttaccatgacagagaagcctctgtccacgttggtgtggagc	581	
Db	2096	gaatttggcttttcgaacgagutlcaacaccgcgtcctcaaaagcttgagacagcttctgcgttacg	2155	
OY	582	cccccgatctgcgcgcccggaagctcttvgaggggaaggagatlgaaagccccagcttgac	641	
Db	2156	cgcacatctgcgcacccgcgagctgtttcagaggcaaaaagtaacgacgagccggaagctgcat	2215	
OY	642	atcttggaacccctgggggtgtgtctaagcttccggtcgtcgttctctccctctgatggg	701	
Db	2216	gttttgcgtcttgggcgtcatccctgtatacgtttaagtcgggtttcccttcccttcgaacg	2275	
OY	702	cctaacccgcgcagctctagacacggtgtctgtagagccgcgtcttcgcacatccctcttc	761	
Db	2276	tccaccttgaaaggagtttgcgtgaaagcgttctccaaaggcaaatatagaattcccttcat	2335	
OY	762	atgtctcaagaactgttgagagccttgatccgcgcgacatgcttgttggatggaccgcgcacg	821	
Db	2336	atgtctgaactgactcgtgaaanaacttgcctccgcaaatctttagtactgaatccgcaagcgt	2395	
OY	822	atcaccatcgtcccgagatcccggaagcaccgcgttggatg	857	
Db	2396	gtcagttctggaanaacatcatctggtgcgacaaagttagtg	2431	
RESULT 12				
AAF85149				
ID	AAF85149 standard; DNA; 4790 BP.			
XX	AAF85149:			
AC				
XX				
DT	09-JUL-2001 (first entry)			
DE	DNA encoding a dishevelled associated kinase (DAK) isoform DAKb.			
XX				
KW	Dishevelled associated kinase; DAK; DAKa; DAKb; DAKc; cell proliferation;			
RN	cancer; ss.			
CS	Homo sapiens.			
XX				
Key	Location/Qualifiers			
FT	CDS 178..3354			

[illegible]

Db 1002 tcactgtgtggt 1013

RESULT 15
AAAF5338 standard; cDNA; 3200 BP.

XX AAF5338;

DT 11-MAY-2001 (first entry)

XX Human TGF-beta receptor cDNA clone HDPGX45.

XX Human; antisclerotic; dermatological; immunosuppressive; cytostatic;
XX antiinflammatory; anti-HIV; immunostimulant; cardiant; vascular;
XX ophthalmological; neuroprotective; nootropic; anticonvulsant; vaccine;
XX antiparkinsonian; antimicrobial; vulnery; gene therapy; infection;
XX transforming growth factor; TGF; TGF-beta receptor; immune disorder;
XX hyperproliferative disorder; cardiovascular disease; angiogenesis;
XX neurological disorder; ss.

XX Homo sapiens.

XX WO200112670-A1.

XX 22-FEB-2001.

XX 10-AUG-2000; 2000WO-US21736.

XX 13-AUG-1999; 99US-0148682.

XX 20-SEP-1999; 99US-0154887.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, NI J;

XX WPI; 2001-202858/20.

XX P-PSDB; AAB71959.

XX Nucleic acid molecules encoding 12 transforming growth factor-beta
XX receptor polypeptides, useful for preventing, diagnosing and treating
XX e.g. cancers, Parkinson's disease and diabetic retinopathy -

XX Claim 1; Page 285-286; 311pp; English.

XX The present sequence is a nucleic acid molecule encoding one of 12 novel
XX human transforming growth factor (TGF)-beta receptor polypeptides. The
XX TGF-beta receptor polynucleotides and polypeptides may be used in the
XX prevention, diagnosis and treatment of diseases associated with
XX inappropriate polypeptide expression. Such diseases include immune
XX disorders (e.g. multiple sclerosis, systemic lupus erythematosus and
XX human immunodeficiency virus (HIV) infections), hyperproliferative
XX disorders (e.g. cancers and Gaucher's disease), cardiovascular diseases
XX (e.g. Schmitzer syndrome, Chaga's cardiomyopathy and coronary
XX arteriosclerosis), angiogenic disorders (e.g. corneal graft
XX neovascularization and diabetic retinopathy), neurological disorders
XX (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease)
XX and infectious diseases. The polynucleotides and polypeptides are also
XX useful for promoting wound healing, regeneration and/or chemotaxis. The
XX polynucleotides and their complementary sequences may also be used as DNA
XX probes in diagnostic assays to detect and quantitate the presence of
XX as antigens in the production of antibodies and in assays to identify
XX modulators of protein expression and activity. The anti-TGF-beta receptor
XX antibodies may be used to down regulate expression and activity and as
XX diagnostic agents for detecting the presence of the polypeptides in
XX samples.

XX Sequence 3200 BP; 727 A; 948 C; 831 G; 694 T; 0 other;

*Query Match

9.0%; Score 227.2; DB 22; Length 3200;

Best Local Similarity 56.3%; Pred. No. 2e-35;
Matches 446; Conservative 0; Mismatches 343; Indels 3; Gaps 1;

OY	65	gaatcaggccgcaagaagccctccgggtgtgttttaccagatcagcgagcccttgg	124
Db	16	gaagcggccaccacacaaacacacccgcgcacccgtagcttctggagacccttgg	75
OY	125	caaaagcaacttcgcggttgtaagctggcgcgcacatcgatcaccaaaacagttgc	184
Db	76	caaaagcaccctacgggaaggtgaagaagcgcgggaagctcgggscgttggccct	135
OY	185	aataaaataattgataaacaacgattagatccaagcaatttggagaaaatctatcgt	244
Db	136	caagtaatccggaaaggacaaatacaagaatgagaagaatctgtagcatatcggagg	195
OY	245	ggtcagctgtagaagcttgaacatcacatcacatcaaaagctttaccagttatga	304
Db	196	gatttgatgatacgtatcatccttaacacccctcaatcatctgcatcagatgaagt	255
OY	305	aacaaagacatgctttatcatcgtcatgtaatttgcataaaatggagaaatgttgat	364
Db	256	gaacagcagcaagatcgtatcgtatgtagatgtagatgcagcggggcgaccttatg	315
OY	365	tttgacttccaaagcgacactgagtgagaacagcgcggaagaatctctgcaatct	424
Db	316	catcagcgagcgcgacagctcagtgagcggaactgaagcatcttctccgagatcgt	375
OY	425	gtcgcgctggagtagctgcaacacatcacatcgtccacgcggagacctaagaacg	484
Db	376	ctctgcgctgcatcttgcacacagaaacagagttgtccacgagatctccaagctg	435
OY	485	cctctgctgtagtgcaacatgagacatcaacagctgcaagatttggatttggaaat	544
Db	436	catcctcttgtagtccaaatggaatatacaagttgtcagctcgccttccaacctta	495
OY	545	caagtcagagagagcctctgtccacgttggttggagcccccgatgtgcgcccgga	604
Db	496	ccatcaaggaagatctcccgcaagacatctctgtggagcccccttatgtctccgca	555
OY	605	cttgaagggaagagatgaagggcccccagctgtagacatctggaacctgggcgtgtg	664
Db	556	tgtaaatgggaagccctacacagcagcaggaagtgtagcaagctggtccctgggt	615
OY	665	gtacgtcctgctgctgggttctctccctcgtatgggcttaacctgcccagcgtga	724
Db	616	ctacatctgtgtgcatlgtgcacacatgccccttggatgcatgataagatccctag	675
OY	725	gggggtgctgagggccgtctccgcatccctcttcatgtctcaagactgtgagacct	784
Db	676	acaagatcagcaacgggctctacccggagcgacacctaaccctctgtgctctgtg	732
OY	785	gacgcgcgcatgtctggtgtagaccgcgacgcaatccatccatgcgcagatccgga	844
Db	733	gacgcgggtggtgttgtagtgaacccaccccgccgggcccactgtgagatgtggcca	792
OY	845	gaaccggtgat 856	
Db	793	tcactgtgtggt 804	

Search completed: March 22, 2002, 13:25:12
Job time: 7055 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 22, 2002, 13:29:28 ; Search time 3748.51 Seconds

(without alignments)
11583.423 Million cell updates/sec

Title: US-09-787-559-4

Perfect score: 2632
Sequence: 1 ccccgagcgacgacgacg.....aaaaaaaaaaaaaaaaaa 2632

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*
1: gb_da:*
2: gb_htg:*
3: gb_in:*
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6: gb_pat:*
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8: gb_pl:*
9: gb_pr:*
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13: gb_un:*
14: gb_vl:*
15: em_ba:*
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32: em_htgo_rtd:*
33: em_htgo_hum:*
34: em_htg_inv:*
35: em_htg_rtd:*
36: em_htg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2632	100.0	2632	6 AX024732	AX024732 Sequence
2	2522.8	95.9	2533	6 AX024729	AX024729 Sequence
3	2326.6	88.4	2361	6 AX166527	AX166527 Sequence
4	1635.8	62.2	4092	10 AF106937	AF106937 Ratus no
5	1609.2	61.1	2650	10 AB020480	AB020480 Ratus no
6	1575.2	59.8	4498	10 MMU01494	MMU01494 Mus muscu
7	1060.2	40.3	5115	5 AF219232	AF219232 Gallus ga
8	509.8	19.4	4868	6 AX086548	AX086548 Sequence
9	509.8	19.4	4868	9 HSM081732	HSM081732 Sequence
10	509.4	19.4	5163	6 AX056393	AX056393 Sequence
11	508.2	19.3	2213	9 AK000396	AK000396 Homo sapi
12	506.4	19.2	148463	2 AC012140	AC012140 Homo sapi
13	506.4	19.2	158063	9 AP001046	AP001046 Homo sapi
14	506.4	19.2	340000	9 AP001751	AP001751 Homo sapi
15	494.4	18.8	179556	2 AC018734	AC018734 Homo sapi
16	466	17.7	4626	9 AB018324	AB018324 Homo sapi
17	389.4	14.8	4460	9 AB023216	AB023216 Homo sapi
18	382.6	14.5	4321	6 AX056387	AX056387 Sequence
19	344.4	13.1	4917	9 AB058763	AB058763 Homo sapi
20	344	13.1	1594	6 AX056390	AX056390 Sequence
21	342.8	13.0	3609	9 AB049127	AB049127 Homo sapi
22	300	11.4	2884	10 AF240783	AF240783 Mus muscu
23	300	11.4	2929	10 AF240782	AF240782 Mus muscu
24	294.2	11.2	2959	10 RNMARK1	RNMARK1 Homo sapi
25	289.6	11.0	2112	9 AF387638	AF387638 Homo sapi
26	289.6	11.0	2701	9 BC008771	BC008771 Homo sapi
27	289.6	11.0	2946	9 HSTPEKEM	HSTPEKEM Homo sapi
28	286.4	10.9	2572	10 RNMARK2	RNMARK2 Homo sapi
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30	285.4	10.8	2271	9 AF387637	AF387637 Homo sapi
31	285.4	10.8	2698	9 HSU64205	HSU64205 Homo sapi
32	283.8	10.6	2914	9 HUMPT8A	HUMPT8A Homo sapi
33	279.2	10.6	3771	3 AF258462	AF258462 Drosophila
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35	279.2	10.6	4790	3 AF387636	AF387636 Drosophila
36	277.2	10.5	2763	10 MMKEM	MMKEM Homo sapi
37	269.8	10.3	170307	3 AC008358	AC008358 Drosophila
38	269.8	10.3	174426	3 AC007710	AC007710 Drosophila
39	269.8	10.3	226773	3 AE003691	AE003691 Drosophila
40	263.8	10.0	2965	9 AF154845	AF154845 Homo sapi
41	263	10.0	6446	3 AF023484	AF023484 Homo sapi
42	257.8	9.8	50010	2 AC014457	AC014457 Drosophila
43	230	8.7	2291	6 AX056394	AX056394 Sequence
44	225.6	8.6	3443	6 AX086949	AX086949 Sequence
45	225.6	8.6	3443	9 HSM081859	HSM081859 Homo sapi

ALIGNMENTS

RESULT 1	AX024732	2632 bp	DNA	15-SEP-2000
LOCUS	AX024732			
DEFINITION	Sequence 4 from Patent WO0017232.			
ACCESSION	AX024732			
VERSION	AX024732.1	GI:10184809		
KEYWORDS				
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
TITLE	1 (bases 1 to 2632)			
JOURNAL	Reinartz,J., Bechtel,M., Kramer,M., Schaefer,B. and Wallich,R.			
FEATURES	Regulatory protein from human keratinocytes			
source	Patent: WO 0017232-A 4 30-MAR-2000;			
	REINARTZ JEANETTE (DE) ; BECHTEL MICHAEL (DE) ; KRAMER MICHAEL (DE)			
	; SCHAEFER BIRGIT (DE) ; WALICH REINHARD (DE)			
	location/Qualifiers			
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	Db	2101	TGCTCCAGTTACAGACACCACCGGCCGCTGCACCGGCGTGCTCCAGAGCCCCCAGCCGG	2160
	Qy	2161	ccccgcccgcttttgatcgcgcccttlytatgaccttggggctctgcgcgtctcccagca	2220
	Db	2161	CCCCGCGCCCGCTTTTGATCGCCCTCTGTGAAGGCCCTGGGGCTCCCGCTGCCAGACA	2220
	Qy	2221	cgcctctcaagtcagggggtcccgctctgctgcgcgcgcccatctccctgaagaccggcgctcc	2280
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	Qy	2461	tccctgtgcagtgagggagcgcctctgacacccctlygacacggacaacttgaactltaagcaataa	2520
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	Qy	2521	cttcaggaagggtgaagaacatctgacctcaaacgaagaacttcttagaagcgaaataag	2580
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	Qy	2581	caatatcattagtggttttggcgaaaaaiaaaaaaaaaaaaaaaaaaaaaa	2632
	Db	2581	CATATCGTTAGGTGTTTTGGCGAAAAIAAAAAAAAAAAAAAAAAAAAAA	2632
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DEFINITION	Sequence 1 from Patent WO0017232.			
ACCESSION	AX024729			
VERSION	AX024729.1	GI:10184808		
KEYWORDS	. human.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Eumalpia; Eutheria; Primates; Carnivora; Hominoidea; Homo.			
TITLE	Reinartz,J., Bechtel,M., Kramer,M., Schaefer,B. and Wallich,R.			
JOURNAL	Regulatory protein from human keratinocytes			
FEATURES	Patent: WO 0017232-A 1 30-MAR-2000;			
source	REINARTZ JEANNETTE (DE) ; BECHTEL MICHAEL (DE) ; KRAMER MICHAEL (DE)			
	; SCHAEFER BIRGIT (DE) ; WALLICH REINHARD (DE)			
	Location/Qualifiers			
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ORIGIN	/organism="Homo sapiens"			
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Best Local Similarity	99.9%; Pred. NO. 0;			
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Db	8	AGGTGCGGCGGAGCCATGTTATCATCTGGAAGTTACGCGGACCCCGGGCGCAAG	67	

[illegible]

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QY 483 ctgagtagaagcagcgcggaagaagtctctgcaaaacctctgcgcgttgagctactgt 542
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Db 361 CTGAGTGAGAACGAGGGCGGGAAGAACTTCTGGCAATCCGCTGGCGGTGAGTACTGCT 420
QY 543 caagacacacacatcgtcaccgagacctcaagaacgaaacctctgtctgtagtgaac 602
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Db 421 CAGGACCATACATCGTCCACCGGGAGCTCAAGACCGAAGACCTCTGCTGATGGGAAC 480
QY 603 atgagacacaaagctgga-----gatttgatttggaattctctcaagtcgga 653
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QY 714 aaggaagtagaagcccccaagctgagacatctgagacctggcgctgtgtactgctc 773
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Db 601 AAGGAGATAGAGGCCCGCCAGCTGGACATCTGAGCCTGGGCGTGTGTACTGCTCTG 660
QY 774 gtctggagttctctccctctgtagtggcctaaccctgacgacgctggaagcagcggtgt 833
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QY 834 gaagggcgcctctgcgaacacctctctcatgtctcaaacgttggaagccttgatccgcgc 893
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QY 894 atgctgtgtgtggaagcccccaagcgacacacacacacacacacacacacacacacac 953
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Db 781 ATCTGTGTGTGGACCCCGCAGCGCATCATCCGAGATCCGAGACACCGGCTGG 840
QY 954 atgcggagctgaagcctctctgacggagacccgctgccccctctctcgacaacagctac 1013
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Db 841 ATGGGGGCTGAGCCCTGCTTGCCGGAGCCGCTGCCCCGCTTCTCCGCAACAGCTAC 900
QY 1014 acctcaaaccttgaggacacatagatgacagcgctgtgtatcatgacagaccttgagctg 1073
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Db 901 ACCTCCAACTGGGCGACATAGATGAGACAGCGCTGGGTATCATGACAGACCTGGGCTG 960
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Db 1081 CCTGCCAGGAGCGCGGCTCGAGACTCGGACTCTCACTGAGTGTGGAGTGCTCTCAGGAA 1140
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Db 1141 GGTCTTCCACGACCTTTCGACCTGCTGCTGTGCCGCGAGCGGACACTTGTGTG 1200
QY 1314 gactcgtctctcagagcgagatgagactgtgagctccagagctctgtctgacgttgacct 1373
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Db 1201 CAGTCCCTCTCAAGGCGGAGATGAGCTGAGCTCCAGAGCTGCTGCAAGTGGCCCTTG 1260
QY 1374 ttcttcgagtgtagtgcacatgacgagagtgcttcgagccccgagcgctgtctcccaag 1433
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Db 1261 TTCTTCCCGGTGATGCTGACGTGACGAGAGTGTTCGGGCCCGGCGCTGTCCCAAGC 1320
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RESULT 4
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DEFINITION AF106937
ACCESSION AF106937.1 GI:6492127
VERSION


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DEFINITION Mus musculus protein kinase mRNA, complete cds.
ACCESSION U11494
VERSION U11494.2 GI:6137751
KEYWORDS
SOURCE house mouse.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Ruiz,J.C., Conlon,F.L. and Robertson,E.J.
TITLE Identification of novel protein kinases expressed in the myocardium
of the developing mouse heart
JOURNAL Mech. Dev. 48 (3), 153-164 (1994)
MEDLINE 95200798
REFERENCE
AUTHORS Ruiz,J.C.
TITLE Direct Submission
JOURNAL Submitted (27-JUN-1994) Joseph C. Ruiz, Molecular and Cellular
Biology, Harvard University, 16 Divinity Ave, Cambridge, MA 02138,
USA
3 (bases 1 to 4498)
REFERENCE
AUTHORS Ruiz,J.C.
TITLE Direct Submission
JOURNAL Submitted (28-OCT-1999) Wells Center for Pediatric Research, Riley
Hospital for Children, Indiana University School of Medicine, 702
Barhill Drive, Room 2616, Indianapolis, IN 46202, USA
REMARK
COMMENT Sequence update by submitter
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VERSION	AF219232.1	GI:6760435	
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	Phasianinae; Gallus.		
REFERENCE	1 (bases 1 to 5115)		
AUTHORS	Xia,Y., Zhang,Z., Kruse,U., Vogt,P.K. and Li,J.		
TITLE	The new serine-threonine kinase, q1k, is a target of the q1n oncogene		
JOURNAL	Biochem. Biophys. Res. Commun. 276 (2), 564-570 (2000)		
MEDLINE	20484194		
PUBMED	11027514		
REFERENCE	2 (bases 1 to 5115)		
AUTHORS	Xia,Y., Zhang,Z., Kruse,U., Vogt,P.K. and Li,J.		
TITLE	Direct Submission		
JOURNAL	Submitted (27-DIC-1999) Molecular and Experimental Medicine, The Scripps Research Institute, 10550 N. Torrey Pines Road, La Jolla, CA 92037, USA		
FEATURES	location/Qualifiers		
source	1..5115		

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RESULT 8
AX086548
LOCUS AX086548 4868 bp DNA PAT 09-MAR-2001
DEFINITION Sequence 500 from Patent WO0112659.
ACCESSION AX086548
VERSION AX086548.1 GI:13275992
KEYWORDS
SOURCE
ORGANISM human.
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
AUTHORS Wiemann, S.
TITLE Human dna sequences
JOURNAL Patent: WO 0112659-A 500 22-FEB-2001;
German Human Genome Project (DE)
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1. 4868
/organism="Homo sapiens"
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BASE COUNT 1279 a 1259 c 1190 g 1140 t
ORIGIN

Query Match 19.4%; Score 509.8; DB 6; Length 4868;
Best Local Similarity 69.5%; Pred. No. 2.2e-85;
Matches 707; Conservative 0; Mismatches 307; Indels 3; Gaps 1;
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QY 214 ggaacctgagcaaaagcgaacttcggtgtgtgaagctggcgcgcaatcgatcccaaaa 273
Db 167 GCACGCTGGGCAAGGGCAACTTCGCTGTGTGTGAAGCTGGGGCGGACCGGATCACCAAG 226
QY 274 cgaggttgcataaataatgtatgaacacgatttgattcaagcaatttgaggaana 333
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QY 334 tctatcgttgaagttcagctgataagcttctgacatccatccacatcataaagctttacc 393
Db 287 TCTACCGAGAAATGATGAATATGAATATGATGATGATGATGATGATGATGATGATGATG 346
QY 394 aggttaatggaacaaagacatgcttacaatcgtaactgaatttgcataaaatgagaaa 453
Db 347 AGGTATGAGAGCAAAATATATGATGATGATGATGATGATGATGATGATGATGATGATG 406
QY 454 tgttgaattatgtacttccacggcgacactgagtgagagcagagcgcgaggaagttct 513
Db 407 TTTTGTACTATCTTGTCTATATCATGCGCGGTTAATATGATGATGATGATGATGATGATG 466
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DEFINITION	HSN801732 4868 bp mRNA PRI 10-MAR-2001
ACCESSION	Homo sapiens mRNA; CDNA DKFZp434K1115 (from clone DKFZp434K1115); complete cds.
VERSION	AL336764
KEYWORDS	AL336764.1 GI:12053044
ORGANISM	human.
REFERENCE	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 4868)
AUTHORS	Wiemann,S., Well,B., Wellenreuther,R., Gassenhuber,J., Glasl,S., Ansojge,W., Boecker,M., Bloeker,H., Battersachs,S., Blum,H., Lauber,J., Duesterhoeft,A., Beyer,A., Koehler,K., Strack,N., Mewes,H.W., Ostenvoelder,B., Obermayer,B., Tampe,J., Heubner,D., Wambutt,R., Korn,B., Klein,M. and Poustka,A. Toward a Catalog of Human Genes and Proteins: Sequencing and Analysis of 500 Novel Complete Protein Coding Human cDNAs Genome Res. 11 (3), 422-435 (2001)
JOURNAL	2 (bases 1 to 4868) Bloeker,H., Boecker,M., Brandt,P., Mewes,H.W., Gassenhuber,J. and Wiemann,S. Direct Submission Submitted (18-JAN-2000) MIPS, Am Klopferspitz 18a, D-82152 Martinsried, GERMANY
REFERENCE	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by GBR (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://www.mips.biochem.mpg.de/proj/cDNA/ .
AUTHORS	Location/Qualifiers
TITLE	1. 4868
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	97. 2877
	/note="KIA0781, 5' extension"
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Query Match	19.4%	Score 509.8;	DB 9;	Length 4868;
Best Local Similarity	69.5%;	Pred. No. 2.2e-85;		
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polya_site	4798			
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ORIGIN				
Query Match	19.4% <td>Score 509.8;<td>DB 9;<td>Length 4868;</td></td></td>	Score 509.8; <td>DB 9;<td>Length 4868;</td></td>	DB 9; <td>Length 4868;</td>	Length 4868;
Best Local Similarity	69.5%;	Pred. No. 2.2e-85;		
Matches 707;	Conservative 0;	Mismatches 307;	Indels 3;	Gaps 1;
polya_signal	4777	.4782		
polya_site	4798			
BASE COUNT	1279 a	1259 c	1190 g	1140 t
ORIGIN				

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RESULT 10
AX056393 5163 bp DNA PAT 13-JAN-2001
LOCUS Sequence 37 from Patent WO0073469.
DEFINITION AX056393
ACCESSION AX056393.1 GI:12229100
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 5163)
AUTHORS Plowman,G.D., Martinez,R., Whyte,D. and Sudersanam,S.
TITLE Protein kinases
JOURNAL Patent: WO 0073469-A 37 07-DEC-2000;
Sugen, Inc. (US)
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RESULT 11
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LOCUS AK000396
DEFINITION Homo sapiens cDNA FLJ20389 f1s, clone KIA4591, highly similar to
AB018324 Homo sapiens mRNA for KIA40781 protein.
ACCESSION AK000396
VERSION AK000396.1 GI:7020457
KEYWORDS oligo capping; f1s (full insert sequence);
SOURCE Homo sapiens; ileal mucosa cDNA to mRNA, clone_11b.kala
clone:KIA4591.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2213)
AUTHORS Tanigami,A., Fujiwara,T., Ono,T., Yamada,K., Fujii,Y., Ozaki,K.,
Hirao,M., Ohmori,Y., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,
Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished (2000)
REFERENCE 2 (bases 1 to 2213)
AUTHORS Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T.,
Shibahara,T., Tanaka,T. and Nakamura,Y.
TITLE Direct Submission
JOURNAL Submitted (15-FEB-2000) to the DDBJ/EMBL/Genbank databases. Sumio
Sugano, Institute of Medical Science, University of Tokyo, Depent of
Virology, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
(E-mail:cdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
Fax:81-3-5449-5416)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing; Research Association for Biotechnology; cDNA library
construction; 5'- & 3'-end one pass sequencing; Departent of
Virology and Human Genome Center, Institute of Medical Science,
University of Tokyo (partly supported by Science and Technology
Agency).
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Best Local Similarity 69.4%; Pred. No. 5,1e-85;
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OY 214 ggaacctgggcaaggaaggaacttcgagtggtgtaagctcgcgcgcgcgcgcgcgcgc 273
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OY 274 cgcaggtgtcaataaataatgatgaataaacagcatatgaattcaagaatttggagaata 333
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OY 394 aggttatggaacaaagagacatgcttacatcgtcactgaattgtctaaatgagagaa 453
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OY 814 cgcgtgaagacggcggtcgtgagagccgccttcacaccccttccttccttccttccttc 873
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OY 1054 tcatgcgaccctggtggtgtagccgagagagcgtgtagtcaactgcgaacacgcgc 1113
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OY 1114 ataacacacttgcgtcattatctaccctcccttcgtgagcgctgaagagatcga 1170
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
TITLE
Homo sapiens, clone RP11-10M14
JOURNAL
Unpublished
2 (bases 1 to 148463)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
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Wesley, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,
Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.
Direct Submission
Submitted (20-OCT-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 30, 2000 this sequence version replaced g1:6454007.
All repeats were identified using RepeatMasker:
http://ftp.genome.washington.edu/RM/RepeatMasker.html
--- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
--- Project Information
Center Project name: L3106
Center Clone name: 10_M_14
--- Summary Statistics
Sequencing vector: M13; M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 135488 bases at least Q40
Consensus quality: 141694 bases at least Q30
Consensus quality: 144517 bases at least Q20
Insert size: 139000; agarose-fp
Insert size: 146863; sum-of-ctgls
Quality coverage: 4.1 in Q20 bases; agarose-fp
Quality coverage: 3.9 in Q20 bases; sum-of-ctgls
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 17 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.

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JOURNAL Submitted (12-JAN-2000) to the DDBJ/EMBL/GenBank databases.
 Nobuyoshi Shimizu, Keio University, School of Medicine, Molecular
 Biology, 35 Shinanomachi, Shinjuku-ku, Tokyo 160-8582, Japan
 (E-mail: nshimizu@med.keio.ac.jp, Tel: 81-3-3351-2370,
 Fax: 81-3-3351-2370)

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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 1 (sites)
 Hattori,M., Fujiyama,A., Taylor,T.D., Watanabe,H., Yada,T.,
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 Yaspo,M.L.

Direct Submission
 Submitted (10-APR-2000) to the DDBJ/EMBL/GenBank databases. The
 Chromosome 21 Mapping and Sequencing Consortium. * RIKEN Genomic
 Sciences Center, Human Genome Research Group * Institute of
 Molecular Biotechnology, Genome Analysis * Keio University School
 of Medicine, Dept. of Molecular Biology * GBF, Dept. of Genome
 Analysis * Max-Planck Institute for Molecular Genetics (addresses
 see below)

On May 30, 2000 this sequence version replaced gi:7717412
 The chromosome 21 mapping and sequencing consortium consisting of
 * RIKEN Genomic Sciences Center, Human Genome Research Group, *
 Sagami-hara 228-8555, Japan,
 * e-mail: hattori@gscl.riken.go.jp
 * URL: http://hgp.gsc.riken.go.jp/
 and
 * Institute of Molecular Biotechnology, Genome Analysis, *
 Deutendbergstrasse 11, D-07745 Jena, Germany,
 * e-mail: gscj-submit@genome.imb-jena.de
 * URL: http://genome.imb-jena.de/
 and
 * Keio University School of Medicine, Molecular Biology, * Tokyo
 160-8582, Japan,
 * e-mail: nshimizu@med.keio.ac.jp
 * URL: http://www.dmb.med.keio.ac.jp/
 and
 * GBF, Dept. of Genome Analysis,
 * Mascheroder Weg 1, D-38124 Braunschweig, Germany, * e-mail:
 info.genome@gbf.de
 * URL: http://genome.gbf.de/
 and
 * Max-Planck Institute for Molecular Genetics,
 * Inhesterrasse 73, D-14195 Berlin, Germany,
 * e-mail: info-chr21@molgen.mpg.de
 * URL: http://chr21.fz-berlin.mpg.de/
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1 (bases 1 to 179556)
REFERENCE
AUTHORS Waterston, R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 179556)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (17-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Jun 16, 2000 this sequence version replaced g1:7023168.

COMMENT
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H_NH0351D02
----- Summary Statistics -----
Sequencing vector: M13: 1008
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Chemistry: Dye-terminator Big Dye; 0% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.90319
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 10 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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* 6731 6830: gap of unknown length
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* 17212 17311: gap of unknown length
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